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OM protein - protein search, using sw model

Run on: October 8, 2003, 17:22:31 ; Search time 55 Seconds
(without alignments)
1477.600 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGSGQAMDGR.....RPEARMPKGTQADVAEVKRF 512

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2706	100.0	512	21	AA197542 Human obesity prot
2	2580.5	95.4	697	21	AAU87087 Human obesity prot
3	2278	84.2	544	23	AAU87087 Human obesity prot
4	2265	83.7	544	20	AAU87087 Human obesity prot
5	2265	83.7	544	21	AAU87087 Human obesity prot
6	2265	83.7	544	22	AAU87087 Human obesity prot
7	2265	83.7	544	24	AAU87087 Human obesity prot
8	2265	83.7	544	24	AAU87087 Human obesity prot
9	2265	83.7	544	24	AAU87087 Human obesity prot

10	2265	83.7	544	24	ABU67464 Human secreted/tra
11	2265	83.7	544	24	ABU61110 Human PRO940 polyp
12	2265	83.7	544	24	ABU65322 Human PRO polypept
13	2265	83.7	544	24	ABU58458 Human PRO polypept
14	2265	83.7	544	24	ABU55994 Human secreted/tra
15	2265	83.7	544	24	ABU56989 Human PRO polypept
16	2265	83.7	544	24	ABU10568 Human secreted/tra
17	2220.5	82.1	639	20	AAU81023 Human sialoadhesin
18	2220.5	82.1	639	21	AAU97543 Human obesity prot
19	2197.5	81.2	639	21	AAU25580 CD33-like protein
20	2142.5	79.2	622	23	AAU87075 Sialic acid-bindin
21	1960	72.4	475	23	AAU87075 Human immunoglobul
22	1929.5	71.3	575	23	AAU87075 Sialic acid-bindin
23	1824	67.4	779	23	AAU87088 Sialic acid-bindin
24	1824	67.4	779	23	AAU87088 Sialic acid-bindin
25	1728	63.9	430	23	AAU87077 Novel human diagn
26	1537.5	55.8	312	22	ABU16067 Novel human diagn
27	1513.5	55.9	686	23	ABU60979 Novel human diagn
28	1507.5	55.7	686	24	AAU34827 Human Silec-12 pr
29	1451	53.6	619	23	AAU87089 Silec-BMS-13a-hig
30	1443	53.3	667	23	ABU60980 Novel human protei
31	1402	51.8	399	20	AAU81024 Human sialoadhesin
32	1290	47.7	563	22	ABU16065 Novel human diagn
33	1101	40.7	525	22	ABU16065 Novel human diagn
34	947	35.0	499	23	AAU21547 Silec8-L protein
35	931	34.4	490	23	ABU53288 Human polypeptide
36	916	33.9	477	23	AAU23674 Silec protein. Und
37	916	33.9	619	23	ABU3287 Human polypeptide
38	915	33.8	272	22	ABU00220 Novel human diagn
39	909	33.6	595	22	ABU70070 Human secreted pro
40	909	33.6	595	23	ABU65509 Human albumin fusl
41	900	33.3	466	23	AAU87078 Sialic acid-bindin
42	888	32.8	431	20	AAU94936 SAF-2 polypeptide
43	888	32.8	431	20	AAU94935 SAF-2 polypeptide
44	879	32.5	463	22	AAU14529 Human novel protei
45	876	32.4	463	22	AAU64077 Human FOAP-9 prote

ALIGNMENTS

RESULT 1
ID AAU97542 standard; Protein: 512 AA.
AC AAU97542:
DT 12-FEB-2001 (first entry)
DE Human obesity protein binding protein-2 homologue #1.
XX
XX
KW Human obesity protein binding protein-2 homologue: HOB-BP2n; obesity;
KW obesity-related disorder; therapy.
XX
XX
OS Homo sapiens.
PN W0200059942-A2.
XX
XX 12-OCT-2000.
XX
XX 22-MAR-2000; 2000WO-US06682.
XX
XX 02-APR-1999; 99US-0127667.
XX
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Su EW, Wei J;
XX WPI; 2000-664992/64.
XX N-PSDB; AAA37847.
XX
XX New human obesity protein binding protein-2 homologue nucleic acids,
PT polynucleotides and polypeptides useful for producing medicament for

PT treating obesity and/or obesity-related disorders
 XX
 PS Claim 9; Page 86-88; 92pp; English.
 XX

CC This sequence is a human obesity protein binding protein-2 homologue
 CC (hob-BP2h) of the invention. The hob-BP2h nucleic acids and polypeptides
 CC may be used for the manufacture of a medicament for the treatment of
 CC obesity and/or obesity-related disorders. The hob-BP2h nucleic acids are
 CC useful as probes or amplification primers in the detection,
 CC quantification or isolation of gene sequences or transcripts, for
 CC recombinant expression of hob-BP2h polypeptides, as immunogens in the
 CC preparation and screening of antibodies, and in sense or antisense
 CC suppression of one or more hob-BP2h genes or nucleic acids, host cell
 CC or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and
 CC polypeptides are useful for raising or screening antibodies that
 CC specifically binds to the hob-BP2h polypeptides.
 CC
 XX Sequence 512 AA;

SO Query Match 100.0%; Score 2706; DB 21; Length 512;
 Best Local Similarity 100.0%; Pred. No. 5.1e-206;
 Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPLLLSSLLGGSGQAMGGRFWIRQESVAVPEGLICISVPCSFSTPRDWTGSTPAYGYW 60
 DB 1 MLPLLLSSLLGGSGQAMGGRFWIRQESVAVPEGLICISVPCSFSTPRDWTGSTPAYGYW 60
 QY 61 FKAVETTKGAPVATNHSREVENSTRKRFQLTGDPKAGNSLVIRDAOMODESQYFFRY 120
 DB 61 FKAVETTKGAPVATNHSREVENSTRKRFQLTGDPKAGNSLVIRDAOMODESQYFFRY 120
 QY 121 ERGSVRYNFMNDGFFLKVTALTKPDDYIPEETLEPGQPVTVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFLKVTALTKPDDYIPEETLEPGQPVTVICVFNMAFECCPPPSFSW 180
 QY 121 ERGSVRYNFMNDGFFLKVTALTKPDDYIPEETLEPGQPVTVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFLKVTALTKPDDYIPEETLEPGQPVTVICVFNMAFECCPPPSFSW 180
 QY 181 TGAALSSOGTKPRTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 DB 181 TGAALSSOGTKPRTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 QY 181 TGAALSSOGTKPRTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 DB 181 TGAALSSOGTKPRTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 QY 241 LVISISRNTDPPRPENLRVMSQANRYLENLNGNSTLPRVLEGOSLCVCVTHSSPPARL 300
 DB 241 LVISISRNTDPPRPENLRVMSQANRYLENLNGNSTLPRVLEGOSLCVCVTHSSPPARL 300
 QY 241 LVISISRNTDPPRPENLRVMSQANRYLENLNGNSTLPRVLEGOSLCVCVTHSSPPARL 300
 DB 241 LVISISRNTDPPRPENLRVMSQANRYLENLNGNSTLPRVLEGOSLCVCVTHSSPPARL 300
 QY 301 SMTORGQVLSQPDPGVLELPRQVEHEGFTGHABHPLGSSQHVSLSLSVHYKKGLIS 360
 DB 301 SMTORGQVLSQPDPGVLELPRQVEHEGFTGHABHPLGSSQHVSLSLSVHYKKGLIS 360
 QY 361 TAFSNGAFLGIGITALLFLCALIMKILPKRRTOTETPRPRFSHSTILDYINVPYAG 420
 DB 361 TAFSNGAFLGIGITALLFLCALIMKILPKRRTOTETPRPRFSHSTILDYINVPYAG 420
 QY 421 PLAQRNOKATPNSRTPRPGAPSPESKKNOKYOLOPSPPEKSSQAPESQSOBEL 480
 DB 421 PLAQRNOKATPNSRTPRPGAPSPESKKNOKYOLOPSPPEKSSQAPESQSOBEL 480
 QY 481 HYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512
 DB 481 HYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512

RESULT 2
 AAU87087
 ID AAU87087 standard; Protein; 697 AA.

XX AAU87087;

XX 05-JUN-2002 (first entry)

XX Static acid-binding Ig-related lectin, Siglec-BMS-L3-995-3.

XX Human; static acid-binding Ig-related lectin; SIGLEC; asthma;
 KW Immune system disease; leukaemia; allergy; inflammatory disease;
 KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;

KW psoriasis; rheumatoid arthritis; conjunctivitis.

XX Homo sapiens.

OS Synthetic.

XX W0200208257-A2.

XX 31-JAN-2002.

XX 20-JUL-2001; 2001WO-US23082.

XX 21-JUL-2000; 2000US-220139P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Longphre M, Chang H, Whitney G;

XX WPI: 2002-241565/29.

DR N-PSDB; ABK43373.

PT Novel isolated SIGLEC (static acid-binding Ig-related lectin) protein
 PT molecules useful for treating immune system diseases such as asthma,
 PT leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease

Example 11; Figure 6; 209pp; English.

CC The invention relates to an isolated SIGLEC (static acid-binding Ig-
 CC related lectin) protein (I). Pharmaceutical compositions comprising (I)
 CC are useful for treating immune system diseases such as asthma, leukaemia
 CC or other allergic or inflammatory diseases. Extracellular domains of (I)
 CC represent potential markers for screening, diagnosis, prognosis,
 CC follow-up assays, and imaging methods. (I) is useful as a target for
 CC drugs which inhibit inflammation, tissue damage and remodeling in
 CC asthma, and inflammatory diseases such as allergic rhinitis,
 CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
 CC conjunctivitis, etc. (I) is also useful for monitoring the course of
 CC disease or disorders, and for identifying agents that bind with and/or
 CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
 CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
 CC methods, and to detect the presence and/or amount of SIGLEC-BMS
 CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
 CC (II) are useful as nucleic acid probes are useful for screening genomic
 CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
 CC number is determined for detecting diseases or disorders associated with
 CC SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
 CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
 CC and in diagnostic imaging technology. AAU87074-AAU87089 represent
 CC human SIGLEC amino acid sequences of the invention.

SO Sequence 697 AA;

Query Match 95.4%; Score 2580.5; DB 23; Length 697;
 Best Local Similarity 73.2%; Pred. No. 6.9e-196;
 Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;

QY 1 MLPLLLSSLLGGSGQAMGGRFWIRQESVAVPEGLICISVPCSFSTPRDWTGSTPAYGYW 60
 DB 1 MLPLLLSSLLGGSGQAMGGRFWIRQESVAVPEGLICISVPCSFSTPRDWTGSTPAYGYW 60
 QY 61 FKAVETTKGAPVATNHSREVENSTRKRFQLTGDPKAGNSLVIRDAOMODESQYFFRY 120
 DB 61 FKAVETTKGAPVATNHSREVENSTRKRFQLTGDPKAGNSLVIRDAOMODESQYFFRY 120
 QY 121 ERGSVRYNFMNDGFFLKVTALTKPDDYIPEETLEPGQPVTVICVFNMAFECCPPPSFSW 180
 DB 121 ERGSVRYNFMNDGFFLKVTALTKPDDYIPEETLEPGQPVTVICVFNMAFECCPPPSFSW 180
 QY 181 TGAALSSOGTKPRTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 DB 181 TGAALSSOGTKPRTTSHFSVLSFTPRPDHDTLCTHVPFSRKGVSAGRTVRLRAYAPRD 240
 QY 241 LVISISRNTD----- 252


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Db 241 LVISISRDNTPALEPPQGNVPLYLEAKGQFLRLLCADSOPATLSWVLQNRVLSSSH 300
QY 253 -----PENLRVAVSOANRTYLE 270
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QY 271 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSWTRQGVLSPPSPDPGVLELPRVOYEHE 330
Db 361 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSWTRQGVLSPPSPDPGVLELPRVOYEHE 420
QY 331 GEFTCHARHPLGSOHVSLSLVHY-----354
Db 421 GEFTCHARHPLGSOHVSLSLVHYSPKLLGPPSCSWAEGLHCSSQASAPSLRWMLGE 480
QY 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGPMANSSLSLHGLSGRLRCFAMVNHGAQSGSILQLPDK 540
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Db 541 KGLISTAFSNGARLIGITALLFLCLALLIMKLLPRRTQETPRPRFSHSTILDYIN 600
QY 416 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKOYOLPSFPEPKSTQAPESOE 475
Db 601 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKOYOLPSFPEPKSTQAPESOE 660
QY 476 SOEELHYATLNFPGVRRPREARMKGTQADYAEVKFQ 512
Db 661 SOEELHYATLNFPGVRRPREARMKGTQADYAEVKFQ 697

RESULT 3
AAU87074 standard: Protein: 544 AA.
ID AAU87074
AC XX
XX XX
DT 05-JUN-2002 (first entry)
DE Stalleic acid-binding Ig-related lectin, Siglec-BMS-13a.
XX XX
KM Human: stalleic acid-binding Ig-related lectin; SIGLEC; asthma;
KM Immune system disease; leukemia; allergy; inflammatory disease;
KM tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
KM psoriasis; rheumatoid arthritis; conjunctivitis.
XX XX
OS Homo sapiens.
XX OS
PN MO200208257-A2.
XX PN
PD 31-JAN-2002.
XX PD
PF 20-JUL-2001; 2001WO-US23082.
XX PF
PR 21-JUL-2000; 2000US-220139P.
XX PR
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PA
PI Longphre M, Chang H, Whitney G;
XX PI
DR WPI: 2002-241565/29.
XX DR
DR N-PSDB; ABK43360.
XX DR
PT Novel isolated SIGLEC (stalleic acid-binding Ig-related lectin) protein
PT molecules useful for treating immune system diseases such as asthma,
PT leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
PT
PS Claim 5; Figure 2B; 209pp: English.
XX PS
XX CC The invention relates to an isolated SIGLEC (stalleic acid-binding Ig-
CC related lectin) protein (I). Pharmaceutical compositions comprising (I)

```

```

CC are useful for treating immune system diseases such as asthma, leukemia
CC or other allergic or inflammatory diseases. Extracellular domains of (I)
CC represent potential markers for screening, diagnosis, prognosis,
CC follow-up assays, and imaging methods. (I) is useful as a target for
CC drugs which inhibit inflammation, tissue damage and remodeling in
CC asthma, and inflammatory diseases such as allergic rhinitis,
CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
CC conjunctivitis, etc. (I) is also useful for monitoring the course of
CC disease or disorders, and for identifying agents that bind with and/or
CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
CC methods, and to detect the presence and/or amount of SIGLEC-BMS
CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
CC (II) are useful as nucleic acid probes are useful for screening genomic
CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
CC number is determined for detecting diseases or disorders associated with
CC SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
CC and in diagnostic imaging technology. AAU87074-AAU87089 represent
CC human SIGLEC amino acid sequences of the invention.
XX CC
XX XX
SQ Sequence 544 AA:
Query Match 84.2%; Score 2278; DB 23; Length 544;
Best Local Similarity 75.1%; Pred. No. 4,9e-172;
Matches 452; Conservative 1; Mismatches 1; Indels 148; Gaps 2;

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Db 61 FKAVETTKAPATNHOSEVEMKSTRGRQLTGDPKAGCSLYIRAOQODSOFYFRV 120
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Db 121 ERGSYRYNFMNDGFLEKVTALQKPDVYIPETLEPQPVTVICVFMAPEECPPPSFW 180
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Db 121 ERGSYRYNFMNDGFLEKVTALQKPDVYIPETLEPQPVTVICVFMAPEECPPPSFW 140
QY 181 TGAALSSQGTPTTSHEVSLSFTPPRODHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 240
Db 181 TGAALSSQGTPTTSHEVSLSFTPPRODHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 240
QY 141 -----VLSFPPRODHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 182
Db 141 -----VLSFPPRODHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 182
QY 241 LVISISRDNTPD-----252
Db 241 LVISISRDNTPD-----252
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Db 183 LVISISRDNTPALEPPQGNVPLYLEAKGQFLRLLCADSOPATLSWVLQNRVLSSSH 242
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Db 253 -----PENLRVAVSOANRTYLE 270
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Db 271 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSWTRQGVLSPPSPDPGVLELPRVOYEHE 330
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Db 303 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSWTRQGVLSPPSPDPGVLELPRVOYEHE 362
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Db 331 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAANSNAGFLIGITALLFLCLALLIMKLLP 390
QY 363 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAANSNAGFLIGITALLFLCLALLIMKLLP 422
Db 363 GEFTCHARHPLGSOHVSLSLVHYKKGLISTAANSNAGFLIGITALLFLCLALLIMKLLP 422
QY 391 KRRTQETTPRPRFSHSTILDYINNVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 450
Db 391 KRRTQETTPRPRFSHSTILDYINNVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 450
QY 423 KRRTQETTPRPRFSHSTILDYINNVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 482
Db 423 KRRTQETTPRPRFSHSTILDYINNVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESK 482
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Db 451 NOKKOYOLPSFPEPKSTQAPESQSEELHYATLNFPGVRRPREARMKGTQADYAEVK 510
QY 483 NOKKOYOLPSFPEPKSTQAPESQSEELHYATLNFPGVRRPREARMKGTQADYAEVK 542
Db 483 NOKKOYOLPSFPEPKSTQAPESQSEELHYATLNFPGVRRPREARMKGTQADYAEVK 542
QY 511 FQ 512
Db 511 FQ 512
QY 543 FQ 544
Db 543 FQ 544

RESULT 4

```

AA41724
 ID AAY41724 standard; Protein; 544 AA.
 XX
 AC AAY41724;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO940 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 XX
 .PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 XX 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
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 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 06-APR-1998; 98US-0081049.
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 PR 21-APR-1998; 98US-0082568.
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 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083332.
 PR 28-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.

PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0083366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0083323.
 PR 13-MAY-1998; 98US-0083338.
 PR 13-MAY-1998; 98US-0083339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 30-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 PI WPI; 1999-551358/46.
 DR N-PSDB; AA234109.
 XX
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders -
 PS
 PS Claim 12; Fig 93; 530pp; English.
 XX
 XX The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA233891 to
 CC AA234338, and AAY41685 to AAY41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 CC
 CC
 XX
 XX Sequence 544 AA;

Query Match 83.7%; Score 2265; DB 20; Length 544;
 Best Local Similarity 74.8%; Pred. No. 5, 2e-171;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSSLLGSGQAMDREMTIRVOESYVWPEGLCTISVPCSFYPRDWTGSTPAYGYW 60
 |||
 Db 1 MLPLLLSSLLGSGQAMDREMTIRVOESYVWPEGLCTISVPCSFYPRDWTGSTPAYGYW 60
 QY 61 FRAVETTKGAPVATNHOSSREVEMSTRGRFOLTGDPKAGNCSLIVIRDAQMDESGYFFRY 120

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Db      61 FKAVTETTKGAPVATNHQSREVEEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRV 120
Qy      121 ERGSYVRYNFMNDGFFLKVATLQKPDVYIPETLEPGQPVTVICVFMWAECECPSPFSW 180
Db      121 ERGSYVRYNFMNDGFFLKVATLQKPDVYIPETLEPGQPVTVICVFMWAECECPSPFSW 180
Qy      181 TGAALSSQGTKPTTSHTSFSVLTFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Db      141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Qy      241 LVISISRDNTPD----- 252
Db      183 LVISISRDNTPALEPOQGNVPYLEAQKGFRLRLCAADSOPTATLSWVLQNRVLSSSH 242
Qy      253 -----PENLRVWVSQANRTVLE 270
Db      243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSQORALDLSVOYPPENLRVWVSQANRTVLE 302
Qy      271 NLGNGTSLPVLEGOGLCVTHSSPPARLSWTORGVLSPOSDPGVLELPRVQYEHE 330
Db      303 NLGNGTSLPVLEGOGLCVTHSSPPARLSWTORGVLSPOSDPGVLELPRVQYEHE 362
Qy      331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 390
Db      363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 422
Qy      391 KRRTQETPRPRSRHSTIIDYINVTAPLQAKRQKATPNSPRPLPPGAPSPSKK 450
Db      423 KRRTQETPRPRSRHSTIIDYINVTAPLQAKRQKATPNSPRPLPPGAPSPSKK 482
Qy      451 NQKKQYQLPSPFPKSTQAPESQESQELHYATLNPFGVRPREARMPKGTQADYAEVK 510
Db      483 NQKKQYQLPSPFPKSTQAPESQESQELHYATLNPFGVRPREARMPKGTQADYAEVK 542
Qy      511 FQ 512
Db      543 FQ 544

RESULT 5
AAB44280
ID      AAB44280 standard; Protein: 544 AA.
AC      AAB44280;
XX
DT      08-FEB-2001 (first entry)
DE      Human PRO940 (UNQ477) protein sequence SEQ ID NO:259.
XX
KM      Human: secreted protein; transmembrane protein; PRO; EST: cytosolic;
KW      expressed sequence tag; detection: cancer.
XX
OS      Homo sapiens.
XX
PN      MO200053756-A2.
PD      14-SEP-2000.
XX
PF      18-FEB-2000; 2000WO-US04341.
XX
PR      08-MAR-1999; 99MO-US05028.
PR      12-MAR-1999; 99US-0123957.
PR      29-MAR-1999; 99US-0126773.
PR      21-APR-1999; 99US-0130232.
PR      28-APR-1999; 99US-0131445.
PR      14-MAY-1999; 99US-0134287.
PR      23-JUN-1999; 99US-0141037.
PR      26-JUL-1999; 99US-0145688.
PR      29-OCT-1999; 99US-0162506.
PR      30-NOV-1999; 99MO-US28313.
PR      02-DEC-1999; 99MO-US28551.
PR      02-DEC-1999; 99MO-US28565.

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PR      16-DEC-1999; 99MO-US30095.
PR      30-DEC-1999; 99MO-US31243.
PR      30-DEC-1999; 99MO-US31274.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00277.
PR      06-JAN-2000; 2000WO-US00376.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI      Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlsen ME;
PI      Goddard A, Godowski PJ, Grimaldi CJ, Gunney AL, Hillan KJ;
PI      Kijavrin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI      Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR      WPI: 2000-611443/58.
DR      N-PSDB: AAC78510.
XX
PT      Novel PRO polypeptides and polynucleotides used in detection methods,
PT      to target bioactive molecules to specific cells, and to modulate
PT      cellular activities -
XX
PS      Claim 12; Fig 93; 636pp; English.
XX
CC      AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC      sequence tag) sequences which encode secreted or transmembrane PRO
CC      polypeptides. The PRO polynucleotides and polypeptides have cytosolic
CC      activity. The PRO polynucleotides and polypeptides can be used for detecting
CC      the presence of PRO polypeptides in samples, for linking bioactive
CC      molecules to cells and for modulating biological activities of cells,
CC      using the polypeptides for specific targeting. The polypeptide targeting
CC      can be used to kill the target cells, e.g. for the treatment of cancers.
CC      The polypeptide pairs provide specific targeting of bioactive molecules
CC      to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC      the isolation of the PRO polynucleotide sequences.
XX
SQ      Sequence 544 AA;

Query Match      83.7%; Score 2265; DB 21; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy      1 MLRLPLLSLILGSGQAMDRFMIRVQESVWMEGLCTVPCSFSPRODMTGSTPAYGYW 60
Db      1 MLRLPLLSLILGSGQAMDRFMIRVQESVWMEGLCTVPCSFSPRODMTGSTPAYGYW 60
Qy      61 FKAVTETTKGAPVATNHQSREVEEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRV 120
Db      61 FKAVTETTKGAPVATNHQSREVEEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRV 120
Qy      121 ERGSYVRYNFMNDGFFLKVATLQKPDVYIPETLEPGQPVTVICVFMWAECECPSPFSW 180
Db      121 ERGSYVRYNFMNDGFFLKVATLQKPDVYIPETLEPGQPVTVICVFMWAECECPSPFSW 180
Qy      181 TGAALSSQGTKPTTSHTSFSVLTFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Db      181 TGAALSSQGTKPTTSHTSFSVLTFTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Qy      141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Db      141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Qy      241 LVISISRDNTPD----- 252
Db      241 LVISISRDNTPD----- 252
Qy      183 LVISISRDNTPALEPOQGNVPYLEAQKGFRLRLCAADSOPTATLSWVLQNRVLSSSH 242
Db      183 LVISISRDNTPALEPOQGNVPYLEAQKGFRLRLCAADSOPTATLSWVLQNRVLSSSH 242
Qy      253 -----PENLRVWVSQANRTVLE 270
Db      253 -----PENLRVWVSQANRTVLE 270
Qy      271 NLGNGTSLPVLEGOGLCVTHSSPPARLSWTORGVLSPOSDPGVLELPRVQYEHE 330
Db      271 NLGNGTSLPVLEGOGLCVTHSSPPARLSWTORGVLSPOSDPGVLELPRVQYEHE 330
Qy      303 NLGNGTSLPVLEGOGLCVTHSSPPARLSWTORGVLSPOSDPGVLELPRVQYEHE 362
Db      303 NLGNGTSLPVLEGOGLCVTHSSPPARLSWTORGVLSPOSDPGVLELPRVQYEHE 362
Qy      331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 390
Db      363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGITALLFLCLALIMKILP 422

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QY 391 KRRTQTEPRPRESRHSITLIDYINVVPTAGLAKRQKATPNSPTPLPGAPSPESK 450
Db 423 KRRTQTEPRPRESRHSITLIDYINVVPTAGLAKRQKATPNSPTPLPGAPSPESK 482
QY 451 NOKKQYOLPSPPEKKSSTOAPESQESQELHYATLNPVGPVPRPEARMKGTQADYAEVK 510
Db 483 NOKKQYOLPSPPEKKSSTOAPESQESQELHYATLNPVGPVPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 6
AAU29082 standard; Protein: 544 AA.
ID AAU29082
XX
AC AAU29082;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #59.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN MO200168848-A2.
XX
PD 20-SEP-2001.
XX
PE 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 28-MAR-2000; 2000US-191314P.
PR 29-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 30-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209833P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.

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PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
PA (GETH ) GENENTECH INC.
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
DR MPI; 2001-602746/68.
XX N-PSDB; AAS45983.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
PS Claim 11; Fig 118; 774pp; English.
XX
CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 544 AA:

Query Match 83.7%; Score 2265; DB 22; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLDPLLSLLGSGQAMDGFRWIRQBSVMPBEGICISVPSFSYPRQDMGTSPAYGYW 60
Db 1 MLDPLLSLLGSGQAMDGFRWIRQBSVMPBEGICISVPSFSYPRQDMGTSPAYGYW 60
QY 61 FKAVETTTGAPVATNHOSEVEMSTGRQRLTDPKAKGCSLYTRQAQODESOYFRV 120
Db 61 FKAVETTTGAPVATNHOSEVEMSTGRQRLTDPKAKGCSLYTRQAQODESOYFRV 120
QY 121 ERGSYVRYNFMNDGFPLKVTALTOKPDVYIPETLEPQAPYVICFENMAFECCPPPSFW 180
Db 121 ERGSYVRYNFMNDGFPLKVT----- 140
QY 181 TGAALSSQGTKPTTSHSVLSFTPRPDHDTDLTCHVDSRRKGVSAQRTVRLVAYAPRD 240
Db 141 -----VLSFTPRPDHNTDLTCHVDSRRKGVSAQRTVRLVAYAPRD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALPEPQGNVPYLEAKQGFLLKCAADSOPATLSWLNQNVSSSH 242
QY 253 -----PPENLRVAVSQANRTVLE 270
Db 243 WGPRLGLELPGVKAGDSGRYTCRAENRRLGSGQRALDLSQYRPENLRVAVSQANRTVLE 302
QY 271 NLGNSTSLPYLEQSLCLVCVYTHSSPPARISWTQRCQVLSPPSQDPGVLELPRVQVEHE 330
Db 303 NLGNSTSLPYLEQSLCLVCVYTHSSPPARISWTQRCQVLSPPSQDPGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSOHSLSLSVYKKGKLISTAFSNGCAFGLIGITALLFLCLALITKTP 390
Db 363 GEFTCHARHPLGSOHSLSLSVYKKGKLISTAFSNGCAFGLIGITALLFLCLALITKTP 422

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OY 391 KRRTQTETPRPRSRHSSTILDYINVPYTAGPLAQKRNOKATPNSPRTPLPPGAPSPESKK 450
    |||||||
Db 423 KRRTQETPRPRSRHSSTILDYINVPYTAGPLAQKRNOKATPNSPRTPPPGAPSPESKK 482
    |||||||
OY 451 NKKKQYQLPSFPEPKSSTQAPESQESQELHATLNPQVRRPPEARMPKGTQADYAEVK 510
    |||||||
Db 483 NKKKQYQLPSFPEPKSSTQAPESQESQELHATLNPQVRRPPEARMPKGTQADYAEVK 542
    |||||||
OY 511 FQ 512
    ||
Db 543 FQ 544

RESULT 7
ABU71170
ID ABU71170 standard; Protein: 544 AA.
AC ABU71170;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human PRO940 protein.
XX
KW Human; PRO; secreted; transmembrane; cytosolic; TNF-alpha; blood;
KM tumour necrosis factor alpha release; chondrocyte cell; proliferation;
XX differentiation; tumour; gene therapy.
OS Homo sapiens.
XX
PN US2003036143-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04342.
PR 24-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05601.
PR 15-MAR-2000; 2000WO-US05841.
PR 30-MAR-2000; 2000WO-US06884.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 28-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-06340P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 28-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 20-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 27-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 31-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 01-APR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 08-APR-1998; 98US-080333P.
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PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081105P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
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PR 22-APR-1998; 98US-082704P.
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PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
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PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
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PR 05-JUN-1998; 98US-088202P.
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PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
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PR	10-JUN-1998;	98US-088824P
PR	10-JUN-1998;	98US-088825P
PR	10-JUN-1998;	98US-088826P
PR	11-JUN-1998;	98US-088861P
PR	11-JUN-1998;	98US-088863P
PR	11-JUN-1998;	98US-088876P
PR	12-JUN-1998;	98US-089090P
PR	12-JUN-1998;	98US-089105P
PR	16-JUN-1998;	98US-089512P
PR	16-JUN-1998;	98US-089514P
PR	17-JUN-1998;	98US-089538P
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QY	61	FKAVETETTKGAPVATNHQSRREVEMSTRGRFQLTGDPAGKNSLVYRDMQODESQYFRRV	120
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QY	121	ERGSYVRYNFPANDQEFELKVTALFQKPDVYIDETLEPGQPVTVICVFMMAFEECPPEPSFW	180
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QY	181	TGAAISSQGTKPTTSHFSVSEFPPODHDITLCHVDESKRGVSAQRTVLRVAYAPRO	240
Db	141	VLSTFRPDQDHTDLTCHVDFSKRGVSAQRTVLRVAYAPRO	180
QY	241	LVTSISNDNTPD-----	252
Db	183	LVTSISNDNTPALEPQGNVPYLEAQKQGFILRLCAADSOPATLSWLVQNRVLTSSHP	240
QY	253	-----PPENLRVWVSQANKRYVLE	270
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QY	271	NLNGTSLPYLEQSILCVTHSSPPARLSWTORGVLSPSPSDPGVLELPRVQYEH	330
Db	303	NLNGTSLPYLEQSILCVTHSSPPARLSWTORGVLSPSPSDPGVLELPRVQYEH	360
QY	331	GEFTCARHPHLSQSHVSLSVHYKKGLISTAANSNAFLGIGTALLFLCLALINKILP	390
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QY	391	KRRTQETPRPRFSRSHSTIIDYINVPYTAGPLAQKRNQKATPNSPRTPLPFGAPSPESKK	450
Db	423	KRRTQETPRPRFSRSHSTIIDYINVPYTAGPLAQKRNQKATPNSPRTPLPFGAPSPESKK	482
QY	451	NOKKQVQLPSFPPKSTQAPAEQSEQSEELHYATLMPGRPRPEARMKGTQADYAEVK	510
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XX	KM	Human; PRO: secreted protein; transmembrane protein;	
XX	KM	cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;	
XX	KM	colon tumour; breast tumour; prostate tumour; rectal tumour;	
XX	KM	cervical tumour; liver tumour; TNF-alpha release; arthritis;	
XX	KM	tumour necrosis factor alpha; chondrocyte cell; bone disorder;	
XX	KM	carriage disorder; sports injury.	
OS	XX	Homo sapiens.	
XX	PN	US2003036156-A1.	
XX	PD	20-FEB-2003.	
XX	PF	02-JUL-2002; 2002US-0188767.	
XX	PR	16-SEP-1998; 98WO-US19330.	
XX	PR	07-OCT-1998; 98WO-US21141.	

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PR 14-MAY-1999; 99WO-US10733.
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Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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DB 61 FKATETTKGAPVATNHSREVENSTRGRFOLITGPARGNCSLYVRDQOMODESIFYFRV 120
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DB 121 ERGSVRYNFMNDGFFLKVLTALTKRPDYIPELTLEPGQPVYICVFNNAFECPPPSFW 180
QY 121 ERGSVRYNFMNDGFFLKVLTALTKRPDYIPELTLEPGQPVYICVFNNAFECPPPSFW 180
DB 121 ERGSVRYNFMNDGFFLKVLTALTKRPDYIPELTLEPGQPVYICVFNNAFECPPPSFW 180
QY 181 TGAALSSQGTPTTSHFSVLSTPRPDHDTDLTCHVDPSRKGVSAGQRTVRLRAYAPRD 240
DB 141 TGAALSSQGTPTTSHFSVLSTPRPDHDTDLTCHVDPSRKGVSAGQRTVRLRAYAPRD 240
QY 241 LVYISRDNTPD-----VLSFTPRPDHNTDLTCHVDPSRKGVSAGQRTVRLRAYAPRD 252
DB 241 LVYISRDNTPD-----VLSFTPRPDHNTDLTCHVDPSRKGVSAGQRTVRLRAYAPRD 252
QY 183 LVYISRDNTALEPQPOGNVYLEAQKGFRLRLCAADSQPPATLSWYLNRYLSSSH 242
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QY 253 -----PPENLRVMTSOANRTVLE 270
DB 243 WGPRLGLELPCVKAAGSGRYTCRAENRLSGOQRLALDSVQPPENLRVMTSOANRTVLE 302
QY 271 NLNGNTSLPVLGEGSLCYVTHSSPPARLSMTORGQVLSPOSPDPVLELPRQVHE 330
DB 303 NLNGNTSLPVLGEGSLCYVTHSSPPARLSMTORGQVLSPOSPDPVLELPRQVHE 362
QY 331 GEFTCHAHPLGSOHVSLSLVHYKKGLISTAFSNGAFLGITALLFLCTALLIMKILP 390
DB 363 GEFTCHAHPLGSOHVSLSLVHYKKGLISTAFSNGAFLGITALLFLCTALLIMKILP 422
QY 391 KRRTOTETPRRFSHSTILYINVPYAGPLAQRNKAAPNSRTPRLPGAPSPESKK 450
DB 423 KRRTOTETPRRFSHSTILYINVPYAGPLAQRNKAAPNSRTPRLPGAPSPESKK 482
QY 451 NOKROYOLPSPPEKSSTOAPESQESQELHYATLNFPGVAPRPRAPKSTQADYAVK 510
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QY 511 FQ 512
DB 543 FQ 544

RESULT 9
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ABU65960;
20-MAY-2003 (first entry)
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Human; secreted protein; transmembrane protein; cytosolic;
gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
adrenal tumour; lung tumour; colon tumour; breast tumour;
prostate tumour; rectal tumour; cervical tumour; liver tumour.
Homo sapiens.
US2003036157-A1.
20-FEB-2003.
02-JUL-2002; 2002US-0188769.
16-SEP-1998; 98WO-US19330.
07-OCT-1998; 98WO-US21141.
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08-MAR-1999; 98WO-US05028.
14-MAY-1999; 99WO-US10733.
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PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090678P.
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PR 25-JUN-1998; 98US-090696P.
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PR 26-JUN-1998; 98US-091010P.
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PR 02-JUL-1998; 98US-091632P.
PR 04-AUG-1998; 98US-094006P.
PR 10-AUG-1998; 98US-095988P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096871P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
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PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
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PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.

Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Oy 1 MLPLLLSLGSGQADGRFWIRQESVWVPEGICISVPCSFYPRQDWTGSTPAYGW 60
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Db 1 MLPLLLSLGSGQADGRFWIRQESVWVPEGICISVPCSFYPRQDWTGSTPAYGW 60
|||||
Oy 61 FKAVETTKGAPVATNHSREVENSTGRGROLTGDPKAGKNCSLVIRDAOMODESOYFRV 120
|||||

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Db      61  FKAATETTKGAPVATNHSREVENMSTRGFRFULTGDPKAGNCSLVIRDAQMODESQYFFRV 120
Oy      121  ERGSYVRNFMNDGFFLVLTALTKPKDYIIPETLEGGQPVYIVICVFNNAFECPPPSW 180
Db      121  ERGSYVTVNFMNDGFFLVLT-----140
Oy      181  TGAALSSQGTPTTSHFSVLSFTPRPDHDTLCTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
Db      141  -----VLSTPRPDHNDTLCTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
Oy      241  LVISISRNDTPD-----252
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Oy      271  NLGNSTSLPYLEGQSLCVYTHSSPPARLSWTORGQVLSPSQDPGVLELPRVQVEHE 330
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Oy      331  GEFTCHAHNPLGSOHVSLSLVHYKKGLISTAFSNGAFLGIGITALFLCLALIMKILP 390
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Oy      391  KRROTETPRPRFSHSTILDIYINVPPTAGPLAQRNKAATPNNSRTLPFGAPSPESKK 450
Db      423  KRROTETPRPRFSHSTILDIYINVPPTAGPLAQRNKAATPNNSRTLPFGAPSPESKK 482
Oy      451  NQKKOYQLSPFPEPKSTQAPESQSOEELHATLNFPGVPRPRAPRKGTQADYAEVK 510
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Oy      511  FQ 512
Db      543  FQ 544

RESULT 10
ABU67464
ID      ABU67464 standard; Protein; 544 AA.
XX
XX      ABU67464;
AC
XX      29-MAY-2003 (first entry)
DT
XX      Human secreted/transmembrane protein (PRO) #59.
DE
XX      Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW      tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KM      tissue typing.
XX
XX      Homo sapiens.
OS
XX      US2003036162-A1.
XX      20-FEB-2003.
PD
XX      12-JUL-2002; 2002US-0194423.
PF
XX      16-SEP-1998; 98MO-US19330.
XX      07-OCT-1998; 98MO-US21141.
XX      01-DEC-1998; 98MO-US25108.
XX      08-MAR-1999; 99MO-US05028.
XX      14-MAY-1999; 99MO-US10733.
XX      02-JUN-1999; 99MO-US12252.
XX      01-SEP-1999; 99MO-US20111.
XX      15-SEP-1999; 99MO-US21090.
XX      01-DEC-1999; 99MO-US28301.
XX      02-DEC-1999; 99MO-US28551.
XX      30-DEC-1999; 99MO-US31274.
XX      05-JAN-2000; 2000MO-US00219.

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PR      18-FEB-2000; 2000MO-US04341.
PR      18-FEB-2000; 2000MO-US04342.
PR      22-FEB-2000; 2000MO-US04414.
PR      24-FEB-2000; 2000MO-US05004.
PR      01-MAR-2000; 2000MO-US05601.
PR      02-MAR-2000; 2000MO-US05841.
PR      15-MAR-2000; 2000MO-US06884.
PR      30-MAR-2000; 2000MO-US08439.
PR      17-MAY-2000; 2000MO-US13705.
PR      22-MAY-2000; 2000MO-US14042.
PR      30-MAY-2000; 2000MO-US14941.
PR      02-JUN-2000; 2000MO-US15264.
PR      28-JUL-2000; 2000MO-US20710.
PR      24-AUG-2000; 2000MO-US23328.
PR      08-NOV-2000; 2000MO-US30952.
PR      01-DEC-2000; 2000MO-US32678.
PR      20-DEC-2000; 2000MO-US34956.
PR      28-FEB-2001; 2001MO-US06520.
PR      01-JUN-2001; 2001MO-US17800.
PR      20-JUN-2001; 2001MO-US19692.
PR      29-JUN-2001; 2001MO-US21066.
PR      09-JUL-2001; 2001MO-US21735.
PR      29-AUG-2001; 2001MO-US27099.
PR      26-JUN-1998; 98US-0105413.
PR      07-OCT-1998; 98US-0168978.
PR      06-NOV-1998; 98US-0187368.
PR      07-DEC-1998; 98US-0202054.
PR      03-MAR-1999; 99US-0254311.
PR      14-MAY-1999; 99US-0311832.
PR      25-MAY-1999; 99US-0380137.
PR      25-AUG-1999; 99US-0380138.
PR      25-AUG-1999; 99US-0380139.
PR      25-AUG-1999; 99US-0380142.
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PR      18-SEP-2000; 2000US-0644610.
PR      18-SEP-2000; 2000US-0665350.
PR      08-NOV-2000; 2000US-0709238.
PR      20-DEC-2000; 2000US-0747259.
PR      12-MAR-2001; 2001US-0816744.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866028.
PR      05-JUN-2001; 2001US-0874503.
PR      18-JUL-2001; 2001US-0908827.
PR      30-JUL-2001; 2001US-0918585.
PR      06-AUG-2001; 2001US-0924419.
PR      13-AUG-2001; 2001US-0929404.
PR      16-AUG-2001; 2001US-0931836.
PR      28-AUG-2001; 2001US-0941892.
PR      04-SEP-2001; 2001US-0946374.
PR      15-JAN-2002; 2002US-0052586.

(GETH ) GENENTECH INC.
XX
XX      Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
PI      Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX      WPI; 2003-332039/31.
XX      N-PSDB; ACA05758.
XX
XX      New secreted and transmembrane PRO polypeptides and nucleic acids,
PT      useful in gene therapy, in chromosome and gene mapping, as chromosome
XX      markers, in tissue typing, and in chromosome identification
XX
XX      Claim 11; Fig 118; 706pp; English.
XX
XX      The invention discloses human nucleic acids encoding secreted and
XX      transmembrane (PRO) polypeptides. Also disclosed is an antibody that
XX      specifically binds to the PRO polypeptide, a method for stimulating the
XX      release of tumour necrosis factor alpha (TNF-alpha) from human blood by
XX      contacting the blood a PRO polypeptide, a method for stimulating the

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CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in AB067406-AB067710 are the PRO polypeptides of the invention.
XX
SQ Sequence 544 AA;
Query Match 83.78; Score 2265; DB 24; Length 544;
Best Local Similarity 74.86; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
QY 1 MLPLLLSLGSGQAMDRFWMIRVOESVWVPEGICISVPCSFSPRODMTGSNPAYGYW 60
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QY 61 FKAIVETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSTVIRDAQODESQYFRRV 120
DB 61 FKAIVETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSTVIRDAQODESQYFRRV 120
QY 121 ERGSYVRNFMNNGEFLKATVIALNOKPDVYIPETILEGPQVYICVFEMAEBCPPSFSW 180
DB 121 ERGSYVRNFMNNGEFLKATVIALNOKPDVYIPETILEGPQVYICVFEMAEBCPPSFSW 180
QY 181 TGAALSSQGTPTTSHEVSLEFTRPODHDITLCHVDFSRKGVSAORTVRLRYAVAPRD 240
DB 181 TGAALSSQGTPTTSHEVSLEFTRPODHDITLCHVDFSRKGVSAORTVRLRYAVAPRD 240
QY 141 -----VSTFTRPODHDITLCHVDFSRKGVSAORTVRLRYAVAPRD 182
DB 141 -----VSTFTRPODHDITLCHVDFSRKGVSAORTVRLRYAVAPRD 182
QY 241 LVISISRDNTPD-----PPENIRVWVSQANRYVLE 252
DB 241 LVISISRDNTPD-----PPENIRVWVSQANRYVLE 252
QY 183 LVISISRDNTPALEPOGNAVPLYLEAQKGQFLRLCAADSQPATISWVLQNRVLSSSH 242
DB 183 LVISISRDNTPALEPOGNAVPLYLEAQKGQFLRLCAADSQPATISWVLQNRVLSSSH 242
QY 253 -----PPENIRVWVSQANRYVLE 270
DB 253 -----PPENIRVWVSQANRYVLE 270
QY 243 WGRPRLGLELPYKACDGRYTCRAENRLGSGQRAILDLSVOYPPENIRVWVSQANRYVLE 302
DB 243 WGRPRLGLELPYKACDGRYTCRAENRLGSGQRAILDLSVOYPPENIRVWVSQANRYVLE 302
QY 271 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSMTORGQVLSPOSDPQVLELPRVOYEHE 330
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DB 423 KRRTQETTPRRPSRSHSTIIDYINVPYTAFLAQKRNQKATPNSPRTLPFGAPSPSKK 482
QY 451 NOKKOYOLPSPFPKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 510
DB 451 NOKKOYOLPSPFPKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 510
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DB 483 NOKKOYOLPSPFPKSTQAPESQESQELHYATLNPGRPRPEAPMPGTADYAEVK 542
QY 511 EQ 512
DB 543 EQ 544
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AB061110
ID AB061110 standard; Protein: 544 AA.
XX AC AB061110;
XX
DT 08-MAY-2003 (first entry)

XX
DE Human PRO940 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW Immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cystostatic; arthritits; tumour; wound healing;
KW genetic disorder; antidiabetic; antidiabetic; antidiabetic;
KW arthritits; anti-tumour; antidiabetic; antidiabetic;
KW cardiant.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-0978697.
XX
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US050190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
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PR 02-MAR-2000; 2000WO-US05841.
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PR 21-MAR-2000; 2000WO-US07532.
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PR 24-AUG-2000; 2000WO-US23328.
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PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06550.
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PR 25-MAY-2001; 2001WO-US17092.
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PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 12-MAR-1998; 98US-077649P.
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PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.

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 PR 30-MAR-1998; 98US-079923P.
 PR 26-MAY-1981; 81US-0267213.
 PR 17-MAR-1998; 98US-0040220.
 PR 26-JUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0168978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187368.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-0218517.
 PR 05-MAR-1999; 99US-0254465.
 PR 10-MAR-1999; 99US-0265686.
 PR 12-APR-1999; 99US-0284291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
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 PR 27-NOV-2000; 2000US-0723749.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0918585.
 XX
 XX (GENENTECH INC.
 XX
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers J, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard N, Godowski PJ, Grimaldi JC, Gurney AL, Hillman KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoi NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
 XX WPI: 2003-288163/28.
 DR N-PSDB; ABX92481.
 DR
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies
 PT
 XX
 PS
 PS Claim 12; Fig 93; 459p; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists. The
 CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, for the genetic
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC AB61071-AB61164 represent the human PRO polypeptides of the
 CC invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at

CC segdata.uspto.gov/psipspidentry.html.
 XX
 SQ Sequence 544 AA:
 Query Match 83.7%; Score 2265; DB 24; Length 544;
 Best Local Similarity 74.8%; Pred. No. 5, 2e-171;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
 QY 1 MLPLLLSLGSGAMGGRFWRQVESYVMEVGLICISYPCFSYPRQDWGCTPAYGW 60
 DB 1 MLPLLLSLGSGAMGGRFWRQVESYVMEVGLICISYPCFSYPRQDWGCTPAYGW 60
 QY 61 FKAVETTKGAPVATNHSREVEVSTRGREFOLGTPANGNCLVYRDAMODESQFFRV 120
 DB 61 FKAVETTKGAPVATNHSREVEVSTRGREFOLGTPANGNCLVYRDAMODESQFFRV 120
 QY 121 ERGSYVRYNFMNDGFELKVTALTOKPDVYIPETLEPGQPVYICVENMAFEBCPPPSFW 180
 DB 121 ERGSYVRYNFMNDGFELKVTALTOKPDVYIPETLEPGQPVYICVENMAFEBCPPPSFW 180
 QY 181 TGAALSSQGTAKPTTSHFVSLSFTPRPDHDDTLTCHVDFSKRGVAQRTVLRVAYARD 240
 DB 141 -----VLSFTPRPDHNDTLTCHVDFSKRGVSAQRTVLRVAYARD 182
 QY 141 -----VLSFTPRPDHNDTLTCHVDFSKRGVSAQRTVLRVAYARD 182
 DB 241 LVISIRNDTPD----- 252
 QY 183 LVISIRNDTPALEPQPGNNPYLEAQGQFLRLCAADSQPPATLSVNLQNVLSSSH 242
 DB 253 -----PPENLRVMSQANRYLE 270
 QY 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSQLALDLSVQYPPENLRVMSQANRYLE 302
 DB 271 NLNGSTSLPYLEGSLCVCYTHSSPPARLSMTORGVLSPQSPDPGLPRVQVHE 330
 QY 303 NLNGSTSLPYLEGSLCVCYTHSSPPARLSMTORGVLSPQSPDPGLPRVQVHE 362
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 QY 363 GEFTCHAHHPGLSGQSVLSLSVHYKKGLISTAFSGALGIGITALLFLCALIIMKILP 422
 DB 391 KRRITQETPPRPFSSHSTILDTINVPYAPGLAQRKNKATPNSEPTLPFGADSPESKK 450
 QY 423 KRRITQETPPRPFSSHSTILDTINVPYAPGLAQRKNKATPNSEPTLPFGADSPESKK 482
 DB 451 NOKKOYOLPSPPEPSSIQAPESQSEDELHYATLNFPGVPRPRAPRMKGGQADYAVK 510
 QY 483 NOKKOYOLPSPPEPSSIQAPESQSEDELHYATLNFPGVPRPRAPRMKGGQADYAVK 542
 DB 511 FQ 512
 DB 543 FQ 544
 RESULT 12
 AB065322 standard; Protein: 544 AA.
 ID AB065322;
 AC AB065322;
 XX
 XX 16-MAY-2003 (first entry)
 DT
 XX
 XX Human PRO polypeptide #59.
 DE
 XX
 KW Human; PRO; cytosolic; chromosome mapping; gene mapping;
 KW protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
 KW chondrocyte differentiation; chondrocyte proliferation; tumour.
 OS Homo sapiens.
 XX
 XX US2003032102-A1.
 PN
 XX
 XX 13-FEB-2003.
 PD
 XX

PF 17-JUN-2002: 2002US-0173697.
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Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5,2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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DB 61 FKAVTETTKGAPVATNHOSEVENSTRGFRFOLTFGPAKNGSLVIRDAQOMODESQFFRV 120
QY 121 ERGSVVRNFMNDGFEFLKVTALTOKPDVYIETLEPGQPTVICVFNMAFECPPEPSFSW 180
DB 121 ERGSVVRNFMNDGFEFLKVTALTOKPDVYIETLEPGQPTVICVFNMAFECPPEPSFSW 180
QY 181 TGAALSSQGTPTTSHFSFVLSFTPRPODHTDLCHVDFSKKGYSAQRTVLRVAYAPRD 240
DB 141 -----VLSFTPRPODHTDLCHVDFSKKGYSAQRTVLRVAYAPRD 182
QY 241 LVISISRNDTDP----- 252
DB 183 LVISISRNDTDPALPQGNVPLYEAQKGQFLRLLCADSPATLSVILQNRVLSSHP 242
QY 253 -----PENIRVMVSQANRTVLE 270
DB 243 WGPRLLELPVKAGDSGRYTCRAENRLGSQLALDLSVQYPPENLRVMVSQANRTVLE 302
QY 271 NLNGTSLPYLEGGSLCVCVTHSSPPARLSMTQRGVLSPSQSDGCVLELPRVQVEHE 330
DB 303 NLNGTSLPYLEGGSLCVCVTHSSPPARLSMTQRGVLSPSQSDGCVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGIGTALLFLCALIIMKILP 390
DB 363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFLGIGTALLFLCALIIMKILP 422

QY 391 KRRTQETPRPFRFSHSHSTILDYINVVPTAGPLAQKRNQKAPNSRPTLPPGAPSPESKK 450
DB 423 KRRTQETPRPFRFSHSHSTILDYINVVPTAGPLAQKRNQKATPNSRPTLPPGAPSPESKK 482
QY 451 NOKKOYOLPSPEPKSSTOAPESQSOEELHYATLNFQGVRRPAPRMPKGTQADYAEVK 510
DB 483 NOKKOYOLPSPEPKSSTOAPESQSOEELHYATLNFQGVRRPAPRMPKGTQADYAEVK 542
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DB 543 FQ 544
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XX ABUS8458;
AC 15-APR-2003 (first entry)
DT 15-APR-2003 (first entry)
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DE Human PRO polypeptide #59.
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KW Human; PRO: cytosolic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;
KW antibody-dependent enzyme mediated prodng therapy.
OS Homo sapiens.
PN US2003027272-A1.
PD 06-FEB-2003.
PE 21-JUN-2002; 2002US-0176492.
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PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
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Query Match 83.7%; Score 2265; DB 24; Length 544;
Best Local Similarity 74.8%; Pred. No. 5.2e-171;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
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DB 61 FRAVETTTGAVATVTHQSRREVEMSTRGRFQTLTGPACNCSLVIRDAOMODESOYFFRV 120
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DB 121 ERGSYVRYNFMNDGFLLKVTALTQKPDVYIPTLEHGGVVTICVNMFAFECPPPSFEM 180
QY 181 TGAALSSQGTKPRTTSHFSVLSFTPRQDHDITLTCVHDSRRKGVSAQRTVRLVAYAPRD 240
DB 141 -----VLSFTPRQDHDITLTCVHDSRRKGVSAQRTVRLVAYAPRD 182
QY 241 LVISISRQNTPD----- 252
DB 183 LVISISRQNTPALPEPOGQNVPEYLAOKGQFLRLCAADSOPTATLSVWLQNRVLSSSH 242
QY 253 -----PPEMLRYMVSAQNRVYLE 270
DB 243 WGPRLGLELPVKAKGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVSAQNRVYLE 302
QY 271 NIGNGTSLPYLEGOSICLVCVTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVEHE 330
DB 303 NIGNGTSLPYLEGOSICLVCVTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVEHE 362
QY 331 GFTCHARRPLGSOHVSLSISVHYKKGLISTAFSGAPLIGITITALLFLCLALLIMKILP 390
DB 363 GFTCHARRPLGSOHVSLSISVHYKKGLISTAFSGAPLIGITITALLFLCLALLIMKILP 422
QY 391 KRRTQETPRPRFSHSHSTILDYINVVPTAGPLAOKRNQKATNSRTPPLPPGAPSPESKK 450
DB 423 KRRTQETPRPRFSHSHSTILDYINVVPTAGPLAOKRNQKATNSRTPPRPPAPSPESKK 482
QY 451 NOKKOYQLPSPPEPKSSIQAPESQSOEELHYATINPGVRRPRAKMKGTQADYAEVK 510
DB 483 NOKKOYQLPSPPEPKSSIQAPESQSOEELHYATINPGVRRPRAKMKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 14
ABU55994
ID ABU55994 standard; Protein; 544 AA.
XX
AC ABU55994;
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DT 26-MAR-2003 (first entry)
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DE Human secreted/transmembrane protein, PRO940.
XX
XX Human; secreted protein; transmembrane protein; PRO;
KW antiarthritic; vulnerary; tumour necrosis factor-alpha;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; arthritis; sports injury.
XX
XX Homo sapiens.
XX
XX OS
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QY 121 ERGSYVYNNMNDGFFLKVATLQKPDVYIPETLEPGQPVYICVFNMAREECPPSFSW 180
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DB 181 TGAALSSQGTTPPTTSHEVSLSFTPRPODHDITLCHVDFSRKGVSAQRTVRLRYAVAPRD 240
QY 141 -----VLSFTPRPODHDITLCHVDFSRKGVSAQRTVRLRYAVAPRD 182
DB 141 -----VLSFTPRPODHDITLCHVDFSRKGVSAQRTVRLRYAVAPRD 182
QY 241 LVISISRDNTPD----- 252
DB 241 LVISISRDNTPD----- 252
QY 183 LVISISRDNTPDLEPOQGNVPLYEAKGQFLRLCAADSOPPATISWLONRVLSSSH 242
DB 183 LVISISRDNTPDLEPOQGNVPLYEAKGQFLRLCAADSOPPATISWLONRVLSSSH 242
QY 253 -----PPENLRVMSQANRTVLE 270
DB 253 -----PPENLRVMSQANRTVLE 270
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QY 423 KRRTOTETPPRPSRSHSTIIDYINVPYTAQLQKRAQKATPNSPRTPLPPGAPSPSSKK 482
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QY 451 NOKKOYOLPSFPEPKSSTQAPESQESQEEHLVATLNFPGVRRPREARMKGTQADVAEVK 510
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KW	Human; PRO; tumour necrosis factor-alpha; blood; cancer;
KM	chondrocyte cell; tumour; adrenal tumour; lung; colon; breast; prostate;
KW	kidney; rectum; cervix; liver; bone disorder; cartilage disorder;
XX	arthritis; sports injury; genetic disorder; antiarthritic; vulnerary.
OS	Homo sapiens.
XX	
PN	US2003027280-A1.
PD	
XX	06-FEB-2003.
FE	20-JUN-2002; 2002US-0176993.
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QY 181 TGAALSSQGTKKPTTSHSFSTFPRPDHDTLCHVDFSKKGSQAQTVLRVAYAPRD 240
Db 141 -----VLSFTPRPDHNTDLCHVDFSKKGSQAQTVLRVAYAPRD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPDLEPQOGNVPYLEAKQGFRLRLCAADSPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVWVSQANRTVLE 270
Db 243 WGPRLGLELPGVKAGDSGRYTCRAENRLSGQRFALDLSVOYPENLRVWVSQANRTVLE 302
QY 271 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSMTORGVLSPQSPDQVLELPRVOYEHE 330
Db 303 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSMTORGVLSPQSPDQVLELPRVOYEHE 362
QY 331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFILGITALFLCLATILMKILP 390
Db 363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFILGITALFLCLATILMKILP 422
QY 391 KRRTOTETPRPRESRHSITIDYINVPYAGPLAOKRNQKATPNSPRPLPPGADSPESKK 450
Db 423 KRRTOTETPRPRESRHSITIDYINVPYAGPLAOKRNQKATPNSPRPLPPGADSPESKK 482
QY 451 NOKKYOLOPSPREKSTOAPESQSOEELHYATLNPVGRPREARMPKQOADVAEVK 510
Db 483 NOKKYOLOPSPREKSTOAPESQSOEELHYATLNPVGRPREARMPKQOADVAEVK 542
QY 511 FQ 512
Db 543 FQ 544

```

Search completed: October 8, 2003, 20:01:58
 Job time : 58 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 19:49:12 : Search time 30 Seconds
(without alignments)
1641.279 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706
Sequence: 1 MLPLLLSLGSGQAMDGR.....REARNPKGTQADVAEVKQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	694	25.6	364	2 A30521	myeloid cell surfa
2	528	19.5	403	2 I52590	m3-B isoform - mo
3	304.5	11.3	626	1 A61084	myelin-associated
4	302.5	11.2	620	2 JH0593	Schwann cell myel
5	295.5	10.9	626	1 BNR73	myelin-associated
6	289.5	10.7	582	1 BNR73	myelin-associated
7	288.5	10.7	637	2 B33785	myelin-associated
8	245	9.1	1594	2 S50065	sialoadhesin - mou
9	227	8.4	862	2 I49583	differentiation an
10	220.5	8.1	868	2 A46512	CD22 homolog/B 1ym
11	206.5	7.6	647	2 A35648	B-cell adhesion pr
12	202.5	7.5	847	2 JH0371	B-cell adhesion pr
13	186	6.9	526	1 A32164	biliary glycoprote
14	184	6.8	402	2 T05062	probable advanced
15	180	6.7	4391	2 A38096	perlecan precursor
16	167	6.2	321	2 JH0395	biliary glycoprote
17	167	6.2	351	2 JH0396	biliary glycoprote
18	167	6.2	417	2 JH0394	biliary glycoprote
19	167	6.2	464	2 C30127	transmembrane carc
20	156.5	5.8	336	2 C27658	pregnancy-specific
21	153	5.7	3707	2 S16252	heparan sulfate pr
22	153.5	5.7	416	1 A42879	advanced glycosyla
23	151.5	5.6	1241	2 T37190	nephritin - human
24	149	5.5	210	2 JCA122	pregnancy-specific
25	149	5.5	538	2 JCA257	vascular cell adhe
26	148.5	5.5	5175	2 T20992	hypothetical prote
27	148.5	5.5	5198	2 T43290	hemiscientin precus
28	147.5	5.5	1906	1 S68235	myosin-light-chain
29	147	5.4	332	2 JN0067	pregnancy-specific

30	144.5	5.3	26926	1 I38344	titin, cardiac mus
31	143	5.3	702	2 A36319	carcinoembryonic a
32	142.5	5.3	1232	2 T43027	neural cell adhesi
33	141.5	5.2	739	2 JN0581	vascular cell adhe
34	141	5.2	402	2 A54312	pregnancy-specific
35	140.5	5.2	392	1 RMHUPD	poliovirus recepto
36	140.5	5.2	417	1 RMHUPA	poliovirus recepto
37	140.5	5.2	428	2 J50032	pregnancy-specific
38	140.5	5.2	428	2 I57486	pregnancy-specific
39	140	5.2	521	2 S34338	biliary glycoprote
40	140	5.2	628	2 I38000	Lutheran blood gro
41	139.5	5.2	419	2 JCA123	pregnancy-specific
42	139	5.1	404	1 I61596	advanced glycosyla
43	138.5	5.1	349	2 A34815	carcinoembryonic a
44	138.5	5.1	495	2 A55181	pregnancy-specific
45	138	5.1	324	2 G43354	pregnancy-specific

ALIGNMENTS

RESULT 1					
A30521					
Myeloid cell surface antigen CD33 precursor - human					
C:Species: Homo sapiens (man)					
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text-change 29-Aug-1997					
C:Accession: A30521					
R:Simmons, D.; Seed, B.					
J. Immunol. 141, 2797-2800, 1988					
A:Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid prog					
A:Reference number: A30521, MUID:89009814; PMID:3139766					
A:Accession: A30521					
A:Molecule type: mRNA					
A:Residues: 1-364 <SIK>					
C:Genetics:					
A:Gene: GDB:CD33					
A:Cross-references: GDB:119762; OMIM:159590					
C:Map position: 19q13.3-19q13.4					
C:Superfamily: Immunoglobulin homology					
C:Keywords: glycoprotein; surface antigen; transmembrane protein					
F:1-17/Domain: signal sequence #status predicted <Sig>					
F:18-259/Domain: extracellular #status predicted <Ext>					
F:260-282/Domain: transmembrane #status predicted <TM>					
F:283-364/Domain: intracellular #status predicted <CYT>					
F:100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted					
Query Match					
Best Local Similarity 32.8%; Pred. No. 4, 3e-40;					
Matches 168; Conservative 59; Mismatches 137; Indels 148; Gaps 8;					
25.6%; Score 694; DB 2; Length 364;					
OY	1	MLPLLLSLGSGQAMDGRFMTIRVOESVNVPRGCLISVPCSFSPRDMTGSTPAYGW	60		
DB	1	MLPLLLPLLMGALMDPRFVLQVDESIVYVGGCLVLCFFHPIPYDDKNSPVHGW	60		
OY	61	FKAIVETTKGAPATNHQSEVEMSTRGRNLTGDPKAGKCSVIRDAOMODESOFPRV	120		
DB	61	FREGALISGDSFPAITKKLLQDEVOETQGRRLGDSRNKCSISTVDARRDGSFFPRV	120		
OY	121	ERGSYVRNFMNDGFILKYALTQKPRDYIPELTLEGQPTVLCVFNMAFEBCPPSPFSM	180		
DB	121	ERGS-TRKYSKPSQLSVNHTDILNHRKILIPGLERGHKNLCSVSMCEGQTPPIFSM	179		
OY	181	TGAAISSQGTKPTTSIFSVLSTFPRQDHDITLCHVDTSRKGVSAQRVRLAVAPRD	240		
DB	180	LSAAPTSLG--PATTHSSVLIITPRQDHTNLTCCVRFAGAGVITERTIQLNVTVPON	237		
OY	241	LVISIRDMTPDPPEMLRVWVSQANRTVLNENGTSLPLLEGQSLCVLGVTHSSPARL	300		
DB	238	PITGIRP-----GDC-----	247		
OY	301	SWTQRCQVLSPPSPDPCVLELPRVQVEHEGEFTCHARPLGSAQVSLSVHYKKGLIS	360		
DB	248	-----SGKQETRAGVV-----	258		


```

Oy      462 PEPKSTQAPESQSEELHYATLNFPGVRPPPEARMPKGTQADYAEVK 510
          : : | | : : | | : : | | | | :
Db      587 -----RGEPELDTLSYSHDL-GKRPRKDSYTLSEETALEYAEIR 624

```

RESULT 4

Schwann cell myelin protein precursor - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: JH0593; PS0356
R:Linkage: C.; Tropea, M.B.; Cameron-Curry, P.; Rossler, J.; Marshak, D.R.; Roder, J.; Le
Neuron 8, 323-334, 1992
A:Title: Molecular characterization of the schwann cell myelin protein, SMP: structural
A:Reference number: JH0593; MUID:92153423; PMID:1739462
A:Accession: JH0593

A:Cross-references: GB:SB311; NID:g245729; PIDN:AB21466.1; PID:g245750
A:Experimental source: spinal cord
A:Note: the species of quail is not identified
A:Accession: PS0356
A:Accession: PS0356

A:Residues:18-33;119-132;135-157;563-566 / x' / 571 <DU1>
C:Comment: This protein is expressed on all external membranes of Schwann cells
C:Superfamily: myelin-associated glycoprotein; Immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
E:1-17/Domain: signal sequence #status predicted <Sig>
E:18-650/Product: Schwann cell myelin protein #status predicted <Sig>
F:33-101/Domain: Immunoglobulin homology <IM>
F:506-533/Domain: transmembrane #status predicted <TM>
F:222,314,331,405,449/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match	11.2%	Score 302.5	DB 2	Length 620
Best Local Similarity	22.4%	Pred. No. 4	7e-13	
Matches 148; Conservative	89;	Mismatches 224;	Indels 199;	Gaps 29

[illegible]

Oy 114 -SoyFFRBERGSIYRIYNFMNDGFLLKLTALTQKPDDIYPETILEPGDPTVITICVFNMAFEE 172
::||| : | : ||| : : : | : ::|
Db 111 AGKYVYFRGLDGIVNQYSF--SEHAELDVMA---APHLEVPHELVAGSGEAELICRPV---DN 163

```

Oy 173 CPP--PSESWTGA--ALSSGQTK-----PTSHSEVLSFMPRPQDHTDITLCHVDSRK 222
    ||| | :||| | | : | | | | : | | |
Db 164 CPPRLRLTLWTGTEELLDPICKERIEDLDSKSLGSLRFRPKEDIGRRVCGCVTFINS 223

```

```
QY 223 GVSQRTVRLRVAYAPR-----DLVISRDNTP-----DP 253
    : | | | | | : | : |
Db 224 SISFOADVGLDVQTEPQVNVGLMPPEVEVEGSDVELGCCAEERPAPLISWFRSEVLRPEP 2833
```

```

OY      254  PENURVMVSOAN-----RTVLEN-----LNGTSLPVLEGOSL 286
          |||:::|          | ||          : || || | : | :
Db      284  GRNIRLLLSNVGPDGGSEFSCVAENRHRGRNRSLOLRVAYAPRAPYNG-SLWVYSSGDPV 342

```

Qy 287 CLVCVTHSSPPARLSWTORGVLSSQSPDPVLELPRVQYEHGEFTCHARHPLGSOHV 346
 : | | | | : : : : : | : : : | | | : | :
 Db 343 SYMCRAESPPAAILTVLRGGKVMAAIYEDVHTMWRPARBEDGCTVSCVENOHGASST 402

```

0Y 347 SLSLSVHYKKGLI-----STA----- 363
    |::|| |:: |
403 SPNTSVEFVPI VT PASPCTAGCNGVLCVMTNSTDCEI VERT PTHVQVOTVCCDPPDPMIA A53

```

```
OY      364 ---SNGAFLGIGIT-----ALFELCALIMKIIPKRRTQTETPPRFSRH----- 406
       |||: ||: | || | : | | : ||
Db      463 PPSDGSISGI-LTLRGPLERLVLCA-----RNRRGTARQLRFHHPGGLVAK 513
```

```

QY 407 ----STLLIYINVPAGLACKRNNKATPPNSPRPLPP-----GAPSPESKKNQ-----4522
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 514 VCPGVGAVNAFALYIAIVCYLSSQRRKKKAGSEVTPVPGPMAGPCGDDPLDLRQCVWMLR 5733
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
QY 453 --KKQQLPSPFPKPSSTAPESQSEDLHATLNFPGVAPREAPRMFKGTQADYAEVK 510
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 574 GAMERKAL----GVVEGSGAP--QETVTPSH-----PYMKP--TKGPLEDPEVAEIR 618
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

```

RESULT 5

myelin-associated glycoprotein precursor long splice form - rat
N/Alternate names: 1b236; brain neuron cytoplasmic protein 3; MAG
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-Feb-1994 #sequence, revision 31-Dec-1989 #text, change 01-Dec-2000
C/Accession: A29028; A94175; A27185; A90886; I56564; I52892; A03138; A23362
R/Label: C; Brown M.A.; Nave, K.A.; Nornberg, A.B.; Quarles, R.H.; Bloom, F.E.; Milner
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A/Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule
N/Reference number: A29028; MUID:87232001; PMID:2436693

A: Molecule type: mRNA
A: Residues: 1-626 <I>A1>
R: Cross-references: GB:116800; NID:q205269; PIRID:AAA1557.1; PID:q205270
R: Acquisti, M.; Roder, J.; Chie, L.S.; Down, J.; Wilkinson, D.; Bayley, H.; Braun, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 600-604, 1987
A: Title: Molecular cloning and primary structure of myelin-associated glycoprotein
A: Reference number: A94175; M01D:87052455; PMID:24332614

A: Molecule type: mRNA
A: Residues: 1-626 <ARQ>
A: Cross-references: GB:M14871; NID:g205267; PIDD:AAA41556.1; PID:g205268
R: Salzer, J.L.; Holmes, W.P.; Colman, D.R.

J. Cell Biol 04, 957-965, 1987
A:Title: The amino acid sequences of the myelin-associated glycoproteins: homology to
A:Reference number: A27185; MUID:87166195; PMID:2435742

A: Molecule type: mRNA
A: Residues: 1-626 <S>A>
A: Cross-references: GB: X05301, NID: g56611, PID: g56612
B: Suttcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.E.

Cell: 07-062, 1503
A: Title: Identifying the protein products of brain-specific genes with antibodies to
A: Reference number: A90836; MUID:83259254; PMID:6347394
A: Accession: A90836

A: Molecule type: mRNA
A: Residues: 'KS', 311-626 <SUT>
A: Cross-references: GB: V01544; GB: U00756; NID: g56879; PIDN: CA24786.1; PID: g818027
A: Experimental source: clone p18236

A;Note: the authors translated the codon CAG for residue 350 as Asn R;Blom, F.E.; Battenberg, E.L.F.; Milner, R.J.; Sutcliffe, J.G. *J. Neurosci.* 5, 1781-1802, 1985

A:Reference number: 156564; PMID:4020419
A:Accession: 156564
A:Status: preliminary; translated from GB/EMBL/DDDB

A:Residues: 'RS', 311-626 <RES>
A:Cross-references: GB:M36702: NID:g203181: PIDN:AAA40831.1: PID:g203182
R:Subcellular localization: J.G.; Milner, R.J.; Bloom, F.E. 1993

A:Title: Cellular localization and function of the proteins encoded by brain-specific
A:Reference number: 152892; MUID:84206577; PMID:6586365
A:Accession: 152892

A: Molecule type: mRNA
A: Residues: 785, 311-626 <FE2>
A: Cross-references: GB:111721; NID:q206780; PIDN:AAA42082.1; PID:q206781

c:Comment: The long form predominates in early postnatal life; alternative splicing predicts the mature protein to begin at residue 100.
c:Comment: The papers cited variously predict the mature protein to begin at residue 100.
c:Genetics:

[illegible]

QY	239	-----RDLYISISRDTPPPENLRVWVSOANRIVL-----	269
Db	272	NSVTMTCRVNSSNPKLTFAVSWFKDGRPLEDELE-OBOOMSKLISHVTDMRGKYRC	330
QY	270	---ENLNGTS-----LPVLEGOSLCVGVYHSSPPA-RLSMQR	305
Db	331	QASNDIGQSESEVELTVHAPRPSRVNHIIIPSAEGOSVELICESLASPSATNTWYHN	390
QY	306	GVYLSRQSPD-PGVLEPRVQVEHNGEFTCAHRPLSGQHV--SLISVHYKKGLISTA	362
Db	391	RKPI---PEDTGEKLRIPKSPWMAAGNSCLAENRLGHGKIDOBAKLDVHAPRAVTV	446
QY	363	FSN 365	
Db	447	IQS 449	
RESULT	11		
A35648			
B-cell adhesion protein CD22 alpha splice form precursor - human			
C:Species: Homo sapiens (man)			
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000			
C:Accession: A35648			
R:Stamenkovic, I.; Seed, B.			
Nature 345, 74-77, 1990			
A:Title: The B-cell antigen CD22 mediates monocytic and erythrocyte adhesion.			
A:Reference number: A35648; MID:90231465; PMID:1691828			
A:Accession: A35648			
A:Molecule type: mRNA			
A:Residues: 1-647 <SRA>			
A:Cross-references: GB:X52785; MID:929778; PIDN:CAA36988.1; PID:929779			
C:Genetics:			
A:Gene: GDB:CD22			
A:Cross-references: GDB:127545; OMIM:107266			
A:Map position: 19q13.1-19q13.1			
C:Superfamily: immunoglobulin homology			
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; transme			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-510/Domain: extracellular #status predicted <EXT>			
F:432-484/Domain: immunoglobulin homology <IMM>			
F:511-529/Domain: transmembrane #status predicted <TM>			
F:530-647/Domain: intracellular #status predicted <CYT>			
F:57,101,112,135,164,231,268,302,397,457/Binding site: carbohydrate (asn) (covalent)			
Query Match	7 6%:	Score 206.5:	DB 2: Length 647:
Best Local Similarity	19.0%:	Pred. No. 1.8e-06:	
Matches 130; Conservative 87; Mismatches 212; Indels 257; Gaps 27;			
QY	1	MLPLLLSLGSGQAMGRFMI-RVQSVVWVPEGLITVPCSPS-----YPRQ	48
Db	3	LLGPLLLLVLEVLAFSDSSKWEFHEPETYLAMGACVWILPCYIRALDGLDFLPHNP	62
QY	49	DWGTGTPAYGVWFAVIETTKGAPVATRNHOSREVENSTKGRFOLTGDPANGSLVIRDA	108
Db	63	EYKNTSKFD--GTRLESTKDKRP-----SEQRVQFLGDKNK-NCTLSIHVY	109
QY	109	QMODESQYFFVERGSYVRYNFMDGFELKVTALTKRPDYIRETLEPGQPVYICVN-	167
Db	110	HLNDSGGLRMES---KTEKMERKHLNVSEPRPPHAIQLPELQESOEYVTLCLNF	165
QY	168	-----WAFECPPPSFSWTGAALSSQGT-----KPTSHFSVLSFTPRPDH	209
Db	166	SCYGYPIOLWLEGVPMROAAVTSLITIKSVFTRSELKFSQWHSNKI-VTQQLDA	224
QY	210	D-----TDLTCHVDFSRKY-----	224
Db	225	DGKFLSNDIYQLVNKKPKVTVTVIONPMPIRGGDTVTJSCNKNSSNPSTVTRYEMKPHCA	284
QY	225	-----SAORTLVRYAAYAPRL-----	241
Db	285	WEPSLGVLEKIQNVGMNTTIIACAACNSWCSWSPALNVQYAPRDVRYRKIKPLSEIHS	344

QY 242 --VISISRONTDPDP-----ENLRVNVSA-----NRVLENT 272
 Db 345 GNSVSLQCDFFSSSHPEVQFEMKNGRLGKESQLNDSISPEDAGSYSCWVNNISGQTA 404
 QY 273 GNGSTSLPVL-----EGOSLCLVCTHSSPPAR-----LSMTORGVLSP 311
 Db 405 SKAMTLEVLXAPRRRLVNSPGDQVMEGKSATLTCSDDAPPVSHYTWMDDNNO----- 458
 QY 312 SOPSDGVLELPRVQVEHEGEFTCAHRLPLGSOHVLSS-LSVHYKKGLISTAFSNGAFIC 370
 Db 459 SLRPHYSOKRLRELVKQHGSAVWCQGTNSVKGKRSPLSTLTYYSPETI-----GRRA 512
 QY 371 IGTALLFLCLALITIKI-----LPKR-RTQETPPRRSRHSTIIDYINNVFTAGPLAO 424
 Db 513 VEGGS-----CLATLILALIGLKLQRKWRKTSOQLOENS-----SCOSFE 554
 QY 425 KRQKATPNSPRTPLPGAPSPESKKKKQKQVLPSPFPKSTQAPESQOEELHYAT 484
 Db 555 VRKKKTR-----RAPLSDG-----PHSLGCT-----NPMEDGISYTT 587
 QY 485 LNFPGVPRPRAPRMPKQTQADVAEVK 510
 Db 588 LRF-----PEMNIPRTGDAESSEMQ 607

RESULT 12

JH0371
 B-cell adhesion protein CD22 beta splice form precursor - human
 N:Alternate names: B-cell membrane protein CD22
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1991 #sequence, revision 30-Sep-1991 #ext-change 31-Jan-2000
 C:Accession: JH0371.1 156171
 R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
 J. Exp. Med. 173, 137-146, 1991
 A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
 A:Reference number: JH0371.1; MID:91086838; PMID:1985119
 A:Accession: JH0371
 A:Molecule type: mRNA
 A:Residues: 1-847 <MIL2>
 A:Cross-references: GB:X59350; NID:936090; PIDN:CAA42006.1; PID:936091
 A:Experimental source: B lymphocyte
 A:Note: the authors translated the codon AAT for residue 358 as Met
 R:Wilson, G.L.; Naefeld, V.; Kozlow, E.; Menninger, J.J.; Ward, D.; Kehrl, J.H.
 J. Immunol. 150, 5013-5024, 1993
 A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
 A:Reference number: 156171.1; MID:93267103; PMID:8496602
 A:Accession: 156171
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <MIL2>
 A:Cross-references: GB:S61375; NID:9385980; PIDN:AAC18956.1; PID:93184492
 A:Gene: GDB:CD22
 A:Map position: 19q13.1-19q13.1
 A:Features: 138/1: 240/1: 359/1: 417/1: 503/1: 591/1: 679/1: 711/2: 804/3
 C:Superfamily: Immunoglobulin homology
 C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <NAT>
 F:346-398/Domain: Immunoglobulin homology <IMM1>
 F:609-661/Domain: Immunoglobulin homology <IMM2>
 F:688-706/Domain: transmembrane #status predicted <TRA>
 F:67,101,112,135,164,231,363,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
 F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match

Best Local Similarity 7.5%; Score 202.5; DB 2; Length 847;
 Matches 98; Conservative 69; Mismatches 182; Indels 117; Gaps 19;

QY 1 MLPLLLSLGSGQAMDRFWI-RVQESVNVPEGICISVPCFS-----YPRQ 48
 Db 3 LIGPWLILVLEYLAFSSDKSWFEPHETLYAWEGACVWIPCTYRALDGLSEFTLEFHP 62

QY 49 DWTGSTPAYGWYKAVETTTKGAPVATNHQSRREVENSTRGRQLTGDPAKNGSLYIRDA 108
 Db 63 EYKNKTSKFD -CTRIYESTKDGKV-----SEQRVQFLDDKNK -NCTLSIHV 109
 QY 109 QMODESQVFFRVERGSGVRYRNFNDGFELKVTALTKRPDYIPEITLPPQVTVICFN- 167
 Db 110 HLNDSQGLRIMES-----KTEKMERIHNLVSRPPPHITOLPEIIOESQVLTCLINF 165
 QY 168 -----WAECECPSPFSWTAALSQGRKPTTSHPSVLSFTRPDQHDPTDLCVH 217
 Db 166 SCYGYPIQLQMLLEGVPMROAAVTSLSL-----TIKSVTRSELKFSQSNHCKIYTCOL 221
 QY 218 -DFSRKGS-----AQRVRLRVAYAPRDLYI-----SISRNTDPDPPE----- 255
 Db 222 QDADGKFLSNDYQLVNLVKKHPTKLEIKVTPSDALVRGDSVYTMCEVSSN-----PEYTV 277
 QY 256 -----NLR-VVAVSANR-----TVLENLNGTS----- 277
 Db 278 SWLKDSTSLKKQNTFTLNLREYVKKQSCGVSDVGRSEEVFLQVYAPESPVQ 337
 QY 278 ---LPVLEGOSLCLVCTHSSP-PARLSMTORGQVLSPSQSPGVLELPRVQVEHEGEF 333
 Db 338 ILHSPAVESQVYFLCMSLANPLPTNYTWYHNKEM---QGRTEEKVHPIKILPMWAGTY 394
 QY 334 TCHARRPLGS--QHVSLSLSVHYKKGLISTAFSNGAFIGITALL 377
 Db 395 SCVAENILGTGCRGPAELDVYPRPKVTIVIGNPMPIREGDTVTL 440

RESULT 13

A32164
 biliary glycoprotein 1 precursor, splice form a - human
 N:Alternate names: transmembrane carcinoembryonic antigen 1 (TMI-CEA); transmembrane
 C:Contents: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice for
 C:Species: Homo sapiens (man)
 C>Date: 20-Apr-2000 #sequence, revision 20-Apr-2000 #ext-change 20-Apr-2000
 C:Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
 R:Hindoa, Y.; Neumaler, M.; Hefta, S.A.; Drexler, Z.; Wegener, C.; Shively, L.; Heft
 Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
 A:Reference number: A32164
 A:Contents: erratum
 A:Accession: A32164
 A:Molecule type: mRNA
 A:Residues: 1-526 <HIN>
 A:Cross-references: GB:J03858; NID:q179439; PIDN:AAA51826.1; PID:q179440
 R:Hindoa, Y.; Neumaler, M.; Hefta, S.A.; Drexler, Z.; Wegener, C.; Shively, L.; Heft
 Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
 A:Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure
 A:Reference number: A94206; MID:88320555; PMID:2457922
 A:Accession: A94206
 A:Contents: annotation
 A:Note: the sequence shown in this reference has been completely corrected in referen
 R:Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elling, J.J.
 J. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mR
 A:Reference number: A92752; MID:89139550; PMID:2537311
 A:Accession: A30127
 A:Molecule type: mRNA
 A:Residues: 1-526 <BAR1>
 A:Cross-references: EMBL:X16354; NID:q37197; PIDN:CAA34404.1; PID:q37198; EMBL:X14784
 A:Experimental source: splice form a
 A:Accession: B30127
 A:Molecule type: mRNA
 A:Residues: 1-319, 'D', 417-526 <BAR2>
 A:Cross-references: EMBL:X14831; NID:q37199; PIDN:CAA32940.1; PID:q37200; EMBL:X14784
 A:Experimental source: splice form b
 R:Barnett, T.R.; Drake, L.; Pickle IT, W.
 Mol. Cell. Biol. 13, 1273-1282, 1993
 A:Title: Human biliary glycoprotein gene: characterization of a family of novel alter
 A:Reference number: A48078; MID:93140765; PMID:8423792
 A:Accession: A48078
 A:Molecule type: mRNA
 A:Residues: 124-141, 'H', 417-526 <BAR3>

A:Cross-references: GB:M76742; NID:g179480; PIDN:AA57142.1; PID:g179481
 A:Experimental source: splice form x
 A>Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIPI:123606)
 R:Hauck, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.
 Eur. J. Biochem. 223, 529-541, 1994
 A>Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene family
 A:Reference number: S45664; MUID:9433343; PMID:8055923
 A:Accession: S45664
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <HAD>
 A:Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
 R:Nedellec, P.; Turbide, C.; Beauchemin, N.
 Eur. J. Biochem. 231, 104-114, 1995
 A>Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
 A:Reference number: S65939; MUID:95354678; PMID:7628460
 A:Accession: S65939
 A:Status: Preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-21 <NED>
 A:Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 R:Khan, W.N.; Fraenksmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A>Title: Identification of three new genes and estimation of the size of the carcinoembryonic antigen precursor amino-terminal region
 A:Reference number: A44476; MUID:93052339; PMID:1427854
 A:Contents: annotation; alignment of related sequences
 C:Genetics:
 A:Gene: GDB:RGP
 A:Cross-references: GDB:127992; OMIM:109770
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal region
 C:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F:1-34/Domain: signal sequence status predicted <SIG>
 F:35-526/Product: biliary glycoprotein 1, splice form a status predicted <MA7A>
 F:35-428/Domain: extracellular status predicted <EXT>
 F:35-319, 'D', 417-526/Product: biliary glycoprotein 1, splice form b status predicted <F:35-141, 'H', 417-526/Product: biliary glycoprotein 1, splice form x status predicted <F:160-217/Domain: immunoglobulin homology <IMM2>
 F:252-301/Domain: immunoglobulin homology <IMM3>
 F:341-398/Domain: immunoglobulin homology <IMM3>
 F:425-454/Domain: transmembrane status predicted <TM>
 F:453-526/Domain: intracellular status predicted <INT>
 F:104, 111, 115, 152, 182, 197, 208, 224, 232, 254, 274, 288, 292, 302, 309, 345, 351, 363, 378, 405, 475/34

Query Match 6.9%; Score 186; DB 1; Length 526;
 Best Local Similarity 21.5%; Pred. No. 3, 5e-05;
 Matches 130; Conservative 80; Mismatches 200; Indels 196; Gaps 31;

QY 5 LLLSLGGSGAMGRVIRVOESVWPEGICISVP-----CSFSYPRDWTGSPAY 57
 DB 19 LLLSLSL-----TWNPPTTAQLTTESMPENVAEGEYLLVHMLPQO-----LF 63
 QY 58 GY-NFKAVETTKGAPVATNHSREVMSTRGRQLGDPAGK-----NCSLVTRDAQ 109
 DB 64 GYSWYKG--ERYVDS-----NQIVGAIIGTQQAIPGPGANSRETITYNASLLIONVT 113
 QY 110 MDESQYFFRYERSGVYRNFMDGFLKVTALTKPDVYIPELLEGQPVTVICVFNMA 169
 DB 114 QNDGFTYLAQY-----IKSLDLYNE-----EATGQHHV-----141
 QY 170 FEEDPPPSFWTGAALSSQGTPTTSHFVSLSTPRQDDHDTLCHVDFSRKVSAGRT 229
 DB 142 -PELPKPS-----ISSNNSNPEYEDKDAV-AFTCEPETDITTYLWIMNQSPLP---189
 QY 230 VRLVAAYAPRDL-VISISRDNTDPDENLRYVYSQANRT--VLENJGNGSLPVL---282
 DB 190 -RLQISGNRTLTLSTLRNDTGPICEIIONPVS-ANRSDPYTLNVTYGGDTPTTISPSDT 247
 QY 283 -----GOSLCLVCTHSSPPARLSWTORGQVLSPOPSDPOVLELPRVQVEHGEFTGHAR 338

DB 248 YRRPQANLSLSCYASNNPDAQSWMLNGFQOSTOE-----LFIPIVNNSGSTTCAN 302
 QY 339 HPL-GSOHVSLSLHYHKKGLISTAFS-----NGAFIGITALLFLCLA 382
 DB 303 NSVTCNRTYV-----KTIIVELSPVAKPOIKASKTIVTGKDSVNL-----CST 350
 QY 383 L---IIMKILPKRRQTETPPRFRSHSTIIDIYINVV-----TAGP 421
 DB 351 NDTGISIMFPKNSLPSEERKMSQGTITLS-INPVAREAGTYWCEVNPISKNSDP 409
 QY 422 LAQKNOKATPNSPPTLPQGA-----PSPESKKN 451
 DB 410 IMLNPNVALPO--ENGSLPGAIGIVGVALVALVALACFLHFGKTRASDQKDLT 467
 QY 452 QKQYOLPSPPEKPSSTO--APESQSEELHYATLNFPGRP-RPARMPK--GTQADY 506
 DB 468 EHK-----PVSNNHODHSNDPPKNKEVYSTLNEAQQPQPTASPSLTATEIY 520
 QY 507 AEVAKFQ 512
 DB 521 SEVRKQ 526

RESULT 14
 709062
 Probable advanced glycosylation end-products receptor precursor - mouse
 N:Alternate names: RAGE
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
 C:Accession: T09062
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; submitted to the EMBL Data Library, October 1997
 A:Description: Sequence of the mouse major histocompatibility locus III region.
 A:Reference number: Z16543
 A:Accession: T09062
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-402 <ROW>
 A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564950
 C:Genetics:
 A:Gene: RAGE
 A:Map position: 17
 A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
 C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
 C:Keywords: receptor; transmembrane protein
 F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 184; DB 2; Length 402;
 Best Local Similarity 23.4%; Pred. No. 3, 4e-05;
 Matches 101; Conservative 46; Mismatches 139; Indels 146; Gaps 20;

QY 100 NCSLVTRDAQMDQESYFFRV--ERGSYRYRNFMDGFLKVTALTKPDVYIPEL-LEP 156
 DB 80 NSLLLPATGIVDEGFEFRATNRKGEKVSRYR-----VRVYQIIPGRKELIDPAASELTA 134
 QY 157 GQPVTV-ICVFWNAFEPCPPPSFW--TGAALSSQGT-----PTSHESVLS-F 202
 DB 135 SVPNKKGTCVSGSY---PAGLSWHMLDCKLLIPGKETLVKEETRRRPETGLTSEL 191
 QY 203 TRPDHDTLCHVDFSRKVSQAQTVRLVAAYAPRDLVISISHDNTPDENLRYVVS 262
 DB 192 TVIPIQGHTPFFSCFS-IGIPRRRLPLNT---APIDL-----RVRRPPEGIGQLLVE 241
 QY 263 QANRTVLENLGNGTSLPVLEGOSLCLVCTHSSPPARLSWTORGVLSPOPSDPOVLEL 322
 DB 242 PEGGI-----VAPGETVTLTCAISQAPPOVWIKDGAFL-PLAPSP--VLLL 286
 QY 323 PRVQVEHGEFTGHARHPLGSOHVSLSLVH-----KKGLISTAFSNGAF 368
 DB 287 PEVGHEDGTYSCVATHPSHQPSRPVYSINVTGDEGDPAGSGSGEGSLTALAIGLT 346
 QY 369 LGIGITALLFLCLAIIIMKILPKRRQTETPPRFRSHSTIIDIYINVVTPAGPLAQRNQ 428

Db	3597	IASGYPTPDISWS-KIDGSLP-----PDSR-----LENNMLLPVVRPDAGTY	3639
OY	494	-----PEARMPKGTQADYA	507
Db	3640	VCTATNRQGVKAFAPHLQVPERVVPYFTQTPYS	3672

Search completed: October 8, 2003, 20:04:14
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 19:40:42 ; Search time 18 Seconds

(without alignments)
1337.648 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLLPLLSLGLGSGQMDGR.....RPEARMPKGTQADYAEVKFO 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2576.5	95.2	697	1	SIIL_HUMAN
2	1513.5	55.9	686	1	SIIL_HUMAN
3	947.5	35.0	499	1	SIIL_HUMAN
4	909.3	33.6	595	1	SIIL_HUMAN
5	909.3	33.6	597	1	SIIL_PANTR
6	873.3	32.3	457	1	SIIL_MOUSE
7	870.3	32.2	453	1	SIIL_HUMAN
8	836.5	30.9	442	1	SIIL_HUMAN
9	832.5	30.8	467	1	SIIL_HUMAN
10	804.5	29.7	551	1	SIIL_HUMAN
11	694.5	25.6	364	1	CD33_HUMAN
12	689.5	25.5	559	1	SIIL_MOUSE
13	528.5	19.5	403	1	CD33_MOUSE
14	303.5	11.2	626	1	MAG_HUMAN
15	302.5	11.2	620	1	SMP_CORJA
16	295.5	10.9	626	1	MAG_RAT
17	288.5	10.7	626	1	MAG_MOUSE
18	268.5	9.9	1709	1	SN_HUMAN
19	245.5	9.1	1694	1	SN_MOUSE
20	227.5	8.4	862	1	CD22_MOUSE
21	202.5	7.5	847	1	CD22_HUMAN
22	198.5	7.3	330	1	CD22_PONPY
23	193.5	7.2	332	1	CD22_PANPA
24	193.5	7.2	332	1	CD22_PANTR
25	186.5	6.9	526	1	CEAL_HUMAN
26	179.5	6.6	402	1	RAGE_RAT
27	179.5	6.6	4391	1	PGBM_HUMAN
28	176.5	6.5	332	1	CD22_GORGO
29	175.5	6.5	1234	1	NPHN_RAT
30	172.5	6.4	403	1	RAGE_MOUSE
31	161.5	6.0	1242	1	NPHN_MOUSE
32	158.5	5.8	335	1	PSG2_HUMAN
33	155.5	5.7	3707	1	PGBM_MOUSE

34	153.5	5.7	416	1	RAGE_BOVIN	028173 bos taurus
35	151.5	5.6	1241	1	NPHN_HUMAN	060500 homo sapien
36	147.5	5.5	1906	1	KMLN_CHICK	P11799 gallus gall
37	143.5	5.3	702	1	CEAL_HUMAN	P06731 homo sapien
38	142.5	5.3	417	1	PVR_HUMAN	P15131 homo sapien
39	141.5	5.2	739	1	VCAI_MOUSE	P29533 mus musculu
40	140.5	5.2	428	1	PSG3_HUMAN	Q16557 homo sapien
41	140.5	5.2	628	1	LU_HUMAN	P50895 homo sapien
42	139.5	5.2	419	1	PSG7_HUMAN	Q13046 homo sapien
43	139.5	5.1	404	1	RAGE_HUMAN	Q15109 homo sapien
44	138.5	5.1	349	1	CEAL_HUMAN	P31997 homo sapien
45	137.5	5.1	521	1	CEAL_MOUSE	P31809 mus musculu

ALIGNMENTS

RESULT 1	SIIL_HUMAN	STANDARD:	PRT:	697 AA.
ID	SIIL_HUMAN			
AC	096LC7; 096G54; 096LC8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Stailic acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-like protein 2).			
GN	SIGLEC10 OR SLG2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RX	MEDLINE-21303047; PubMed-11409878;			
RA	Yousief G.M., Orlon M.H., Fousias G., Diamandis E.P.;			
RT	"Molecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SLG2) with three splice variants.";			
RL	Biochem. Biophys. Res. Commun. 284:900-910(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Splicein;			
RX	MEDLINE-21181584; PubMed-11284738;			
RA	Floyd J., Kerr S., Ni J., Cornish A.L., Zhang J.Q., Nicoll G.,			
RT	Munday H., Mattei M.-G., Moore P., Liu D., Crocker P.R.;			
RL	"Identification, characterization and leucocyte expression of Siglec-10, a novel human stailic acid-binding receptor.";			
RN	Biochem. J. 355:489-497(2001).			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Dendritic cell;			
RA	MEDLINE-21359381; PubMed-11358961;			
RT	Li N., Zhang W., Wan T., Zhang J., Chen T., Yu Y., Wang J., Cao X.;			
RL	"Cloning and characterization of Siglec-10, a novel stailic acid binding member of the Ig superfamily, from human dendritic cells.";			
RN	J. Biol. Chem. 276:28106-28112(2001).			
RP	SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6.			
RX	MEDLINE-22152890; PubMed-12163025;			
RA	Kitzig F., Martinez-Barriocanal A., Lopez-Botet M., Sayos J.;			
RT	"Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1.";			
RL	Biochem. Biophys. Res. Commun. 296:355-362(2002).			
RN	[5]			
RP	SEQUENCE OF 334-697 FROM N.A. (ISOFORM 1/3/4).			
RC	TISSUE=B-cell;			
RX	MEDLINE-22388257; PubMed-12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RT	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RL	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hultyn S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3- or
 CC 2,6-linked sialic acid. The sialic acid recognition site may be
 CC masked by cis interactions with sialic acids on the same cell
 CC surface. In the immune response, may act as an inhibitory receptor
 CC upon ligand induced tyrosine phosphorylation by recruiting
 CC cytoplasmic phosphatase(s) via their SH2 domain(s) that block
 CC signal transduction through dephosphorylation of signaling
 CC molecules.
 CC -1- SUBUNIT: Interacts with PRPN6/SHP-1 upon phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4);
 CC Secreted (isoform 5).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Long;
 CC IsoId-Q961C7-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short, SV1;
 CC IsoId-Q961C7-2; Sequence=VSP_002565;
 CC Name=3; Synonyms=SV3;
 CC IsoId-Q961C7-3; Sequence=VSP_002564;
 CC Name=4; Synonyms=SV4;
 CC IsoId-Q961C7-4; Sequence=VSP_002561;
 CC Name=5; Synonyms=SV2;
 CC IsoId-Q961C7-5; Sequence=VSP_002562, VSP_002563;
 CC -1- TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes
 CC (eosinophils, monocytes and a natural killer cell subpopulation).
 CC Isoform 5 is found to be the most abundant isoform. Found in lymph
 CC node, lung, ovary and appendix. Isoform 1 is found at high levels
 CC and isoform 2 at lower levels in bone marrow, spleen and spinal
 CC chord. Isoform 2 is also found in brain. Isoform 4 is specifically
 CC found in natural killer cells.
 CC -1- DOMAIN: Contains an intracytoplasmic motif referred as
 CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
 CC is involved in downmodulation of cellular functions as the
 CC termination of the immune response. The phosphorylated ITIM motif
 CC binds to the SH2 domain of PRPN6/SHP-1.
 CC -1- PTM: Tyrosine-phosphorylated
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
 CC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AY029277; AAK40255.1; -
 DR EMBL: AY029277; AAK40256.1; -
 DR EMBL: AF310233; AAK55139.1; -
 DR EMBL: AF311905; AAK92542.1; -
 DR EMBL: AY032685; AAK51124.1; -
 DR EMBL: BC009955; AAK09955.1; -
 DR Genbank: HGNC:15620; SIGLEC10.
 DR MIM: 606091; -
 DR InterPro: IPR007110; Ig-1like.

DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_3.
 DR SMART: SM00409; IgC_2.
 DR SMART: SM00408; IgC_4.
 DR PROSITE: PS00835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Phosphorylation; Alternative splicing;
 KW Polymorphism.
 FT SIGNAL 1 16
 FT CHAIN 1 697
 FT DOMAIN 17 550
 FT TRANSMEM 51 571
 FT DOMAIN 572 697
 FT DOMAIN 18 121
 FT DOMAIN 146 231
 FT DOMAIN 251 339
 FT DOMAIN 344 441
 FT SITE 595 600
 FT SITE 665 670
 FT DISULFID 36 173
 FT DISULFID 41 101
 FT DISULFID 164 215
 FT DISULFID 276 323
 FT DISULFID 380 425
 FT MOD_RES 667 667
 FT CARBOHYD 100 100
 FT CARBOHYD 355 355
 FT CARBOHYD 364 364
 FT CARBOHYD 486 486
 FT CARBOHYD 504 504
 FT VARSPLIC 125 214
 FT VARSPLIC 140 185
 FT VARSPLIC 186 697
 FT VARSPLIC 141 198
 FT VARSPLIC 445 539
 FT MUTAGEN 667 667
 FT CONFLICT 28 28
 FT CONFLICT 134 134
 FT CONFLICT 226 226
 FT CONFLICT 334 336
 FT CONFLICT 344 344
 FT CONFLICT 440 440
 FT CONFLICT 587 587
 FT CONFLICT 625 625
 SQ SEQUENCE 697 AA; 76619 MW; 6CB231CE4911D1B CRC64;
 Query Match 95.2%; Score 2576.5; DB 1; Length 697;
 Best Local Similarity 73.0%; Pred. No. 1; he-173;
 Matches 509; Conservativity 1; Mismatches 2; Indels 185; Gaps 2;
 QY 1 MLPLLSLLSGSQAMDGRFWRVQESYVMEVGLGICISVCSFSYPRODMSTPAYGW 60
 DB 1 MLPLLSLLSGSQAMDGRFWRVQESYVMEVGLGICISVCSFSYPRODMSTPAYGW 60
 QY 61 FRAVETTTGAPVAINHOSREVEKSTRGFQLTGPDPANGCSLVTRDAQMDQESQYFFRV 120
 DB 61 FRAVETTTGAPVAINHOSREVEKSTRGFQLTGPDPANGCSLVTRDAQMDQESQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFLKVTALTKRQDVYIPETLEPGQPVYVYCVNNAFECPPSPSW 180
 DB 121 ERGSYVRYNFMNDGFLKVTALTKRQDVYIPETLEPGQPVYVYCVNNAFECPPSPSW 180
 QY 121 ERGSYVRYNFMNDGFLKVTALTKRQDVYIPETLEPGQPVYVYCVNNAFECPPSPSW 180
 DB 121 ERGSYVRYNFMNDGFLKVTALTKRQDVYIPETLEPGQPVYVYCVNNAFECPPSPSW 180


```

Db      182  TGAALSPKRTPTSTSHFSVLSFTPPSQDHDITDLTCHVDFSRKGVSAQRTVRLRVAAYAKPD 241
Qy      241  LVYSISRNDTPD----- 25
Db      242  LIIISHNDTSALELQGNVILYLEVOQGQFLRLLCADSQPAPYLTSMVLODRYLSSSHPWG 301
Qy      253  -----PPENLRVWVSQANFTYLENTL 272
Db      302  PRITGLBELRGVAGDSGRYTCRAENRLGSOQOALDLSVQYPPENLRVWVSQANFTYLENTL 361
Qy      273  GNGTSLFVLEBGSILCTVCVTHSSPPARLSMTORGOVLSOPOSDPGVLELRLRVQVHEHGE 332
Db      362  GNGTSLFVLEBGSILRYCVTHSSPPARLSMTWMOGTVPBQSDPGVLELRLPIOMHEGE 421
Qy      333  FTCHARRHPLGSONYSLTSLVHYKKGCLISTAFS----- 364
Db      422  FTCHARRHPLGSONYSLTSLVHYPPROLPGSCSMEAGLHCSCSSQASPAPSLRWMLGEEL 481
Qy      365  ----- 364
Db      482  LEGNSGGSFEVTPSSAGRPWANSLSLHGGLSGRLRCAMWNHGAQSSVPOLLPGKL 541
Qy      365  -----NNAFLGIGTALLFTCLALITIMKTLPRKRROTETPRPFSRHSHTIDYINVP 417
Db      542  EHGGGLGLGALAGAGVALLAFCSGLVYFVKICRK-----EARRRAAAG-----DVS 591
Qy      418  TAGPLAQRNOKATPVSPTPLPRCAPSPESKKNOXOKOYOLPSPREPCKSSTQAPESQSO 477
Db      592  TLGPISQGHQHCMSAGSSQDHPBA-----ATYPPGKGEO 628
Qy      478  EELHYATLMPGVPRPRAPRARKPKGTQADYAEVK 510
Db      629  -ELHYASTLSFOGLRMPADQEAASSTYEYSIK 660

```

RESULT 3

ID	SIL8_HUMAN	STANDARD;	PRT;	499 AA
AC	Q9NYZ4.			

28-FEB-2003 (Ver. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sec)

DE Stialic acid binding Ig-like lectin 8 precursor (Siglec-8)
DE (Stal)adhesin family member-3 (STARD3)

Homo sapiens (Human).

NCBI_TaxID=9606; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=30549037. PubMed 11005000

"Molecular characterization of a siglec8
RT
Diamandis E.P.,
G.M.,
Rouse G.,

RL Blochem. Biophys. Res. Commun. 278:775-781(2000).

MEDLINE=20314554; PubMed=10856141;

D'Alessio K.J., Holmes S.D., Abramo
Murdoch P.R., Tachimoto H., Schlett

mast cells, and basophils."

SEQUENCE FROM N.A. (ISOFORM 3).

MEDLINE=20092847; PubMed=10625619;
Floyd H Ni T Connolly J

cygneto: a novel eosinophil-specific member of the immunoglobulin superfamily.¹¹

RL J. Biol. Chem. 275:861-866 (2000).
BN [4]

RA
Floyd H., Zhang J.Q., Crocker

-1- FUNCTION: Putative adhesion molecule that mediates cell-cell dependent binding to collagen.

static acid recognition site may be masked by cis interactions

CC - SUBCELLULAR LOCATION: Type I membrane protein
CC - ALTERNATIVE PRODUCTS:

CC Name=1; Synonyms=Long;
CC Test=Covered 1

```
CC      name=Z;  
CC      ISold=Q9NYZ4-2; Sequence=VSP 002559.
```

Isoid=Q9NYZ4-3; Sequence=VSP_002560;
TISSE=SPCTETTMV

domain contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif

termination of the immune response.

-|- SIMILARITY: BELONGS TO THE MOTIVATIONAL AND EMOTIONAL

-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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EMBL: AF287892: AAC00573 1: -

DR	AF195092	-
EMBL	AA027622.1	-
EMBL	AA027622.1	-

DR genew; HGNC:10877; SIGLEC8.
DR MIM; 605639; -;

GO: GO:0005530; F:lectin; TAS.
GO: GO:0004888; F:lectin; TAS.

InterPro; IPR007110; Ig-like.

DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig: ?

PROSITE; PS50835; IG_LIKE; 2.

SIGNAL 1 16 POTENTIAL

DOMAIN	17	363	EXTRACELLULAR (POTENTIAL).
TRANSMEM	364	384	
INTRACELL	384	384	

383	DOMAIN	499	CYTOPLASMIC (POTENTIAL).
40	DOMAIN	123	IG-LIKE V-TYPE.

DOMAIN	IG-LIKE C2-TYPE 2.
246	344
445	450
SITE	TETV MOETD

T		
DISULFID	42	SAME-LINE MOLIF.
DICHLORIDE	181	BY SIMILARITY.

1	DISOLFID	1/5	224	BY SIMILARITY.
1	DISULFID	283	328	BY SIMILARITY.

CARBOHYD	249	(GLCNAC. . .)	(POTENTIAL).
CARBOHYD	249	N-LINKED	(GLCNAC. . .)
CARBOHYD	249	(GLCNAC. . .)	(POTENTIAL).

1 245 ALTHRPDILILGTLES GHSRNLTCSPWACKQGT PPMISWI
VANSPLC 152

FT	CARBOHD	230	230	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHD	290	290	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHD	360	360	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHD	367	367	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHD	385	385	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	VARSPLIC	4	141	LILLIPLEGICRGAKRQKDYLLTMRKSTYVOEGCLVSVLC	SFSPQGWTPASPRGHGMYRTGRADHDVSRKNIPATNNPARAV
FT					OEETRFDFHILGDPOUNKDCTLSITRDRESDGVNCPVBERG
FT					NMKRNKYVDQLSYNV -> PLTMANERDSGGWADPRFS
FT					(1n isoform short).
FT					/FPid=VSP_002566.
FT					P -> T (in dBSNP:2034891).
FT					/FPid=VAR_014259
SO	SEQUENCE	595 AA;	64984 MM;	D05662176274C5C3 CR664;	
SEQ					
Query Match		33.6%;	Score 909;	DB 1;	Length 595;
Best Local Similarity		43.1%;	Pred. No. 1.7e-56;		
Matches 211;	Conservative	65;	Mismatches 174;	Indels 40;	Gaps 10;
QY	7	LSLLSLGSGQMDIRFEWIRVOESVMVEGICISPCGSFSPRDDMTGSIPTAYTWKRAYTE	66		
Db	137	LSNVNVAASODLSRYLRILEVPESVTVOEGLCVSQSVLTPPHNMWASSPVYGSMKECAD	196		
QY	67	TTYGAFAVNTHOSREVENSTEMSTRGFOLTDGPAGNGSIVYTRDAQOMDESQYFFRVYRGSYV	126		
Db	197	IPMDIYAANTPSGSKVOEDTHGRFLLDGPQNNCSLSIRARKGDSCKYTFQYVERGSR-	255		
QY	127	RYNFMNDGEFLKVTTALTKQEDVIYEPTLEPGQPATVICENMAEFECPPSPSFSGTAALS	186		
Db	256	KMWIYIDKLSVHYTALITHMPRTSIFGTLESCHPNMLTCSVACOGTGPTITMVGASYS	315		
QY	187	SGGTAFYTISHFSVLSETPRRPDHDDTLNCYHDFSRSKGYSAORVTVLYRAVAPRDLYISIS	246		
Db	316	S--LDPTITRRSMLSIIPOQDHGHSILNQVYLPEAGVTIMRAVKLNIST-----	363		
QY	247	RONTDOPRNPLRVMSQAQRVYLEMGSTSLPYLGOSLCLVCYTHSSPPARLSWTORG	306		
Db	364	-----PQNLTMTVFQGDGSTATTLRNGSALSVLEGOSTHLVAVDNSNPAPRLSWTMG	417		
QY	307	OVLSPGPSDPGVELLPVRQVEHEGEFFGNRHHPGSGHVHSLSYNHK--KLISTAF	363		
Db	418	LTLSFGSSNIGLVLETLPVRVHKMBDEEFFCRQANPLGSHGISLSLSDONETGKKMRPIISGV	477		
QY	364	SNGARFLGIGITALFLCLALLIMKILPKRRQTQETPPRPRSRSHTIDYINVV---PTAG	420		
Db	478	TUGAAGGAGAVALFLFYCIIFVYV---RSCRKKSABPAVGVDGTGMEDANAVRGASQSG	534		
QY	421	PLAQKRNGKATPNPSRPRLP--CAPSPESKKNOKKOYQLSPFEPRSSSTAQAESQESQJ	478		
Db	535	PLI-----ESPADDSPPHNAFALTPSPDE-----EGELIYASLSFHKAARPQYEOEDA-I	584		
QY	479	ELHATYATLNEP	488		
Db	585	GYESSEINIP	594		
RESULT 5					
STILL_PANTR					
ID	STILL_PANTR	STANDARD;	PRT;	597 AA.	
AC	Q95LHO;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Slialic acid binding Ig-like lectin-like I precursor (Siglec-				
DE	like molecule 1) (Siglec-1L).				
GN	Sliglecl1.				
OS	Pan troglodytes (Chimpanzee).				
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.				
OX	NCBI_TaxId=9598;				
RN	[1]				
XP	SEQUENCE FROM N.A.				
X	MEDLINE=2153976; PubMed=11546777;				

Query Match	Score 909; DB 1; Length 597;
Best Local Similarity 41.4%; Pred. No. 1,7e-56;	
Matches 212; Conservative 70; Mismatches 164; Indels 66; Gaps 11	
7 LSSLGSGQAMGRFRIRKQESVMPBELCLISVCSFSYPKDMTGSTPAYGYWFAVTE 66	
139 LSNVNTASODLLSRFLVPEBSVYQDELCAVSPCVSLYPHCWMTASSPYVGSMEFKEGAD 198	
67 TTGCAVATAHNHSREYEMSTGRFQFLJDDDPKAKGCSLIVDAQMOQESQFFRYVENGSTV 126	
199 IPDDIPVAINTPSPGKAVQEDTQGRFLLLADDPOTNNCSLSITIDARKGDSGKRYFVERGSR- 257	
127 RINEMNDGEFLKVTALTKQKPVYIPETLPEQAPVTVCENMAFEDRPPPSFMTGAALS 186	


```

Query Match      32.3%; Score 873; DB 1; Length 467;
Best Local Similarity 38.9%; Pred. No. 4,2e-54;
Matches 203; Conservative 74; Mismatches 171; Indels 74; Gaps 11;

OY 2 LLLPSSLLGSGAMGR-----FWLRQESVWPEGLCISVPCSESYPRQ--DWTGS 53
DB 1 MLLLLLLLLMGKIGVGQNPQVEFTLTVRKRKVVQGLCVLPNCNFSYLKRLDWTDS 60
OY 54 TPAGYWKAVETETTKAPVATNHSREVSMTGRGROLGDAKGCSTVDAQMODE 113
DB 61 DPVHGFYREGTBRKNSIVATNNPIKAKVETRNFFELGDAWRNCSINTIEIRKKA 120
OY 114 SQFFRYRGRSYRYKPNMDFLKTALTOKPDVYIPELTPEGPVYICVFNNAFEBC 173
DB 121 GLTFEFLERGR-TKYNMMDKMTLVYALTNPQILLPELTLEAGHSNLTCSVPMCCGVT 179
OY 174 PPFSFWTGAALSSQGRKPTTSHFVSLSFPRRODDDTLTCGVDSRKGVSQKRVAR 233
DB 180 APPIFWMTGHSVFLSTNTGS--SVLTTPQPDHGTMLTCQVTLPGTVSTRMTTRLN 237
OY 234 VATAPDLYTISIRDTPPPELNRVWVSQANRTVLENGTSLPVEGQSICLYCVTH 293
DB 238 VSYAPK-----NLVTIYQADSVSTILKNSSLPISGQSLRLICSTD 281
OY 294 SSPARLSWTQRQGVLSPOSPDGVLELPRQVHEGEFTCHARRPLGSHVSLSVH 353
DB 282 STVPANLSMWNLTLCPSKLSKPGLEFPVHLKGVYVTOAOHALGSHISLSLSPQ 341
OY 354 YKGLISTAFSNGAFIGITALLFLCLALIMKILPKRRQTE---TPRRFRHSIT 409
DB 342 SSATL--SEMMAGTEFGSCVTLALLFVLCILLAVRSYRKARAVANRHP----- 391
OY 410 LVIYINVPAGLACKRKNKATPNRPRLPGADSPESKKNOKKOYLPSFPEKSSSTO 469
DB 392 -DALKYSQNPVLSQADS-----SPLPSILEA 421
OY 470 APEQSQDELHYATLNFPGVRRPEARNPKGTADYEVKR 511
DB 422 ABSSTE--EIHVATLSHEMKPM-NLMGQDITTEYSIKF 460

RESULT 7
SIL9_HUMAN
ID SIL9_HUMAN STANDARD; PRT; 463 AA.
AC Q9Y336; Q9BY19;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Static acid-binding Ig-like lectin 9 precursor (Siglec-9) (FOAP-9 protein).
GN SIGLEC9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=2036134; PubMed=10903842;
RA Zhang J.Q., Nicoll G., Jones C., Crocker P.R.;
RT "Siglec-9, a novel static acid binding member of the immunoglobulin
RL superfamily expressed broadly on human blood leukocytes.";
RN J. Biol. Chem. 275:22121-22126(2000).
RP [3]
RP SEQUENCE FROM N.A. AND MUTAGENESIS OF ARG-120.
RC TISSUE=Peripheral blood;
RX MEDLINE=20357334; PubMed=10801860;
RA Angata T., Varki A.;
RT "Cloning, characterization, and phylogenetic analysis of siglec-9, a
RT new member of the CD33-related group of siglecs. Evidence for
RT co-evolution with static acid synthesis pathways.";
RN J. Biol. Chem. 275:22127-22135(2000).
RN [4]
RP SEQUENCE FROM N.A. AND VARIANT GLU-315.
RA Takayama K., Fujii Y., Tsuritani K., Naitou K., Kawaguchi A., Ukai Y.,
RA Amemiya C., Yajima Y., Yazaki M.;
RT "Molecular cloning of a novel gene, FOAP-9, which are induced by
RT oxidized LDL in human macrophages.";
RN Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillgen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
RA Dangnan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andrade S., Trankheim M., Altix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4."
RT Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Putative adhesion molecule that mediates static-acid
CC dependent binding to cells. Preferentially binds to alpha2,3- or
CC 2,6-linked static acid. The static acid recognition site may be
CC masked by cis interactions with static acids on the same cell
CC surface.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes
CC (neutrophils and monocytes but not eosinophils). Found in liver,
CC fetal liver, bone marrow, placenta, spleen and in lower levels in
CC skeletal muscle, fetal brain, stomach, lung, thymus, prostate,
CC brain, mammary, adrenal gland, colon, trachea, cerebellum, testis,
CC small intestine and spinal cord.
CC -1- DOMAIN: Contains an intracytoplasmic motif referred as
CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
CC is involved in downmodulation of cellular functions as the
CC termination of the immune response.
CC -1- SIMILARITY: BELONGS TO THE IMUNOGLOBULIN SUPERFAMILY. SIGLEC
CC (STATIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: A0135027; AAD26428.2; -
CC EMBL: AF247180; AAF87223.1; -
CC EMBL: AF227924; AAF71455.1; -
CC EMBL: AB026265; BAB41100.1; -
CC EMBL: AC011473; AAG23261.1; -
CC Genew: HGNC:10878; SIGLEC9.
CC MIM: 605640; -
CC
CC GO: GO:0005887; C: integral to plasma membrane; NAS.
CC GO: GO:0005530; F: lectin; NAS.
CC GO: GO:0007166; P: cell surface receptor linked signal transdu. . .; NAS.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam: PF00047; Ig; 3.
CC SMART: SM00409; Ig; 2.
CC PROSITE: PS50835; IG_LIKE; 3.
CC Cell adhesion. Lectin; Antigen; Transmembrane; Signal; Glycoprotein;
CC Immunoglobulin domain; Repeat; Polymorphism.
CC SIGNAL 1
CC 17
CC POTENTIAL.

```

FT	CHAMN	18	463		STATIC ACID-BINDING IG-LIKE LECTIN 9.
FT	DOMAIN	18	348		EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	349	369		POTENTIAL.
FT	DOMAIN	370	463		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	20	140		IG-LIKE V-TYPE.
FT	DOMAIN	146	229		IG-LIKE C2-TYPE 1.
FT	DOMAIN	236	336		IG-LIKE C2-TYPE 2.
FT	SITE	431	436		ITIM MOTIF.
FT	SITE	454	459		SLAW-LIKE MOTIF.
FT	DISULFID	36	170		BY SIMILARITY.
FT	DISULFID	41	102		BY SIMILARITY.
FT	DISULFID	164	213		BY SIMILARITY.
FT	DISULFID	272	320		BY SIMILARITY.
FT	CARBOHYD	101	101		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	138	138		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	161	161		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	225	225		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	231	231		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	238	238		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	256	256		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	CARBOHYD	334	334		N-LINKED (GLCNAG. . .) (POTENTIAL).
FT	VARIANT	100	100		K -> E (1n dbsNP:2075803j).
FT	VARIANT				/FtId-VAR_014254.
FT	VARIANT	125	125		S -> N (1n dbsNP:300658).
FT	VARIANT				/FtId-VAR_014255.
FT	VARIANT	147	147		N -> K (1n dbsNP:273687).
FT	VARIANT				/FtId-VAR_014256.
FT	VARIANT	315	315		A -> E (1n dbsNP:2256983j).
FT	VARIANT				/FtId-VAR_014257.
FT	VARIANT	316	316		A -> D (1n dbsNP:273688).
FT	VARIANT				/FtId-VAR_014258.
FT	MUTAGEN	120	120		R->K: LOSS OF STATIC ACID BINDING.
FT	CONFLICT	269	269		R -> H (1n REF.2)
SO	SEQUENCE	463 AA;	50081 MW;		807BDCED018191F2 CRC64;

Query Match	32.2%	Score 870	DB 1	Length 463
Best Local Similarity	39.4%	Pred. No. 6.7e-54		
Matches 203	Conservative 77	Mismatches 169	Indels 66	Gaps 12
QY	5	LLLSLLGGSGAMDRF--RIWQESVMYRGGLCSIVGCSFSYPRQDTGSPF-AUYGMF	61	
Db	3	LLLLPLGLGRGASQGTSLKLTMQSSVTVGGSLGVNHCSPSYSPENGIYDGRVHGYWF	62	
QY	62	KAVETTKGAFAVATNNHOSREVENSTRGRFOLTGRPAKNCSLVITDAMODESQYFFRYE	121	
Db	63	REGANTODADVAANPNPRAVMEETRDGFHLLGPRHTNCSTLIDARSDAGRTFFRME	122	
QY	122	RGSYVRVFNMDGFEFLKLTALTKQPDVYIPELPEGRQVTVYGVENMAFEEDCPFSFMT	181	
Db	123	KGS-IKNNYKHNRLSVANTALDHNRPNIILPTELSGCGQNLTCSVPACSEGTSPMISVI	181	
QY	182	GAALSSQGTKEFTSHFSVLSFTPRPRQDHTDLTCHYDSRKGVSAQRTVRLVAYAPRDL	241	
Db	182	GTYSVP--LPBSTTRSSVLTLEIPQDQHGSLTCQVTPRGASVTTNKVHLNVSY-----	234	
QY	242	VVISRQNTPRPENLRVMSQARTVLENGISLVLVEGOSLVC---YHTSSPPA	298	
Db	235	-----PQULNTVVGQGTSTVLGNSGSLPKEQSRLTCAVADAVDSNPA	283	
QY	299	RLSWTORGOVLPSPQSDPGVLELRVOVEHEGEFTCHARRPLSOHSLSLVYAKKGL	358	
Db	284	RLSLSMRGILTCPSQSPNPGVLELRPMVHLRADEFTCAQNPDLGQYLVNLQSK---	340	
QY	359	ISTAFNSGAFIGITITALLFTCLALLIMKILPKRRTQETETRPERSRISTLIIDYINV--	416	
Db	341	ATSCVTVGVGVGAGCATALVELFSCVIFVY---SSCRKKSAPRAGVADGTGIEDNAARG	397	
QY	417	-PTAGPLAQKRNOKATPNSRPTPLPGAPSPESKKNOKQYOLSPFEPKSSTOPAESOE	475	
Db	398	SASGQPLTEPMAEDS-----PPDQPPASAR-----SSV	426	
QY	476	SOELRLATLVLPFVYRPRPEAKMRGTDADYAELK	510	

DB	427	GESELOQZASLSFQWKPDR-DSRGGEADPTDEXSEIK	460
RESULT 8			
ID	SIL6_HUMAN	STANDARD:	PRT: 442 AA.
AC	043699;	015388;	043700;
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	15-SEP-2003	(Rel. 42, Last annotation update)	
DE	Stialic acid binding Ig-1-like lectin 6 precursor (Siglec-6) (Obesity-		
DE	binding protein 1) (OB-BP1) (CD33 antigen-like 1).		
GN	SIGLEC6 OR CD33L1 OR OBBP1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RC	TISSUE=Placenta;		
RA	MEDLINE=98127055; PubMed=9465907;		
RA	Takel Y., Sasaki S., Fujiwara T., Takahashi E., Muto T., Nakamura Y.;		
RT	"Molecular cloning of a novel gene similar to myeloid antigen CD33 and		
RT	its specific expression in placenta.";		
RL	Cytogenet. Cell Genet. 78:295-300(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH LEP.		
RC	TISSUE=Erythrocyte;		
RC	MEDLINE=99357812; PubMed=10428856;		
RA	Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,		
RA	Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,		
RA	Varki A., Kastelein R.A.;		
RT	"OB-BP1/Siglec-6. A lectin- and stialic acid-binding protein of the		
RT	immunoglobulin superfamily.";		
RL	J. Biol. Chem. 274:22729-22738(1999).		
RN	[3]		
RP	ERRATUM.		
RA	Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,		
RA	Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,		
RA	Varki A., Kastelein R.A.;		
RL	J. Biol. Chem. 274:28058-28058(1999).		
CC	-1- FUNCTION: Putative adhesion molecule that mediates stialic-acid		
CC	dependent binding to cells. Binds to alpha2,6-linked stialic acid.		
CC	The stialic acid recognition site may be masked by cis interactions		
CC	with stialic acids on the same cell surface.		
CC	-1- SUBUNIT: Interacts with LEP.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);		
CC	Secreted (isoform 2).		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event=1; Alternative splicing; Named isoforms=2;		
CC	Name=1; Synonyms=Membrane-bound, CD33L1;		
CC	Isoid=043699-1; Sequence=Displayed;		
CC	Name=2; Synonyms=Secreted, CD33L2;		
CC	Isoid=043699-2; Sequence=VSP_002553, VSP_002554;		
CC	Note=Should not be confused with SIGLEC5 which has been called		
CC	CD33L2;		
CC	-1- TISSUE SPECIFICITY: Expressed at high levels in placenta (cyto-		
CC	and syncytiotrophoblastic cells) and at lower levels in spleen,		
CC	peripheral blood leukocytes (predominantly B-cells) and small		
CC	intestine.		
CC	-1- DOMAIN: Contains an intracytoplasmic motif referred as		
CC	Immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif		
CC	is involved in downmodulation of cellular functions as the		
CC	termination of the immune response.		
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC		
CC	(SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.		
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.		
CC	-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		

Db 238 Y-----PONTLVTVFQEGEFTASTALGNSSSLVLEGSLRLVCAVDNS 281
 QY 296 PARLSWTORGQVLPSPQSPDGVLELPVROVHEEFGCHAHHPGSHVSLSTVHK 355
 Db 282 PPARLSWTMRSLTLRPSQSPNPVLEL-QVHLDEGEFTCRQNSLGSQVSLNLSLOE 340
 QY 356 -----KGLITAFNSNGAFILGITALFLCLALILIMILPKRRRTQETPPRRSRMS 407
 Db 341 YTGKMRPVSGVLL-----GAVGGAGATLVLFSLFCVITV---RSCRKKSARP----- 386
 QY 408 TILDYINVTAPGLAOKRQKRTPSRPRLPRGAPSPESKKNQKQYQDPSFPKSS 467
 Db 387 -----AADVDIDMK-----DANTIRGSASQCNLTESWADNPRHH 422
 QY 468 TQAPESQSEQLHATLVNFPVPRPEARMKPGTQADYAEVK 510
 Db 423 GLAAHSSGEREITQVAPLSEFHNGEP-DLSGGEATNNERSEIK 464

RESULT 10

SIL5_HUMAN STANDARD: PRT; 551 AA.
 AC 015389;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Stalle acid binding Ig-like lectin 5 precursor (Siglec-5) (Obesity-binding protein 2) (OB binding protein-2) (OB-BP2) (CD33 antigen-like 2) (CD170 antigen).
 GN SIGLECS OR OBBP2 OR CD33L2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Macrophage;
 RX MEDLINE=98402360; PubMed=9731071;
 RA Coriath A.L., Freeman S., Forbes G., Ni J., Zhang M., Cepeda M., Gentz R., Augustus M., Carter K.C., Crocker P.R.;
 RT "Characterization of siglec-5, a novel glycoprotein expressed on myeloid cells related to CD33.";
 RL Blood 92:2123-2132(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Erythroleukemia;
 RX MEDLINE=99357812; PubMed=10428856;
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C., Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F., Varki A., Kastelein R.A.;
 RT "OB-BP1/Siglec-6, A leptin-and stalle acid-binding protein of the immunoglobulin superfamily.";
 RL J. Biol. Chem. 274:22729-22738(1999).
 RN [3]
 RP ERBATOV.
 RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C., Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F., Varki A., Kastelein R.A.;
 RL J. Biol. Chem. 274:28058-28058(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lamerin J.E., McCreedy P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stiliwgen S., Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J., Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Atellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of a 5-Mb region in 19g13.4.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Putative adhesin molecule that mediates stalle-acid dependent binding to cells. Binds equally to alpha2,3-linked and

CC alpha2,6-linked stalle acid. The stalle acid recognition site may be masked by cis interactions with stalle acids on the same cell surface.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed by monocyte/myeloid lineage cells. Found at high levels in peripheral blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing early stages of myelomonocytic differentiation.
 CC -!- DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (STALLE ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF170484; AAD50978.1; -.
 CC EMBL; U71383; AAB70703.1; -.
 CC EMBL; AC018755; AAF87846.1; -.
 CC Genew; HGNC:10874; SIGLECS.
 CC MIM; 604200; -.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_C2.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00408; IGC2; 1.
 CC PROSITE; PS50835; IG_LIKE; 3.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
 CC Immunoglobulin domain; Repeat; Polymorphism.
 CC KW STGNAL 1
 CC FT CHAIN 17 551
 CC FT DOMAIN 17 441
 CC FT TRANSMEM 442 462
 CC FT DOMAIN 463 551
 CC FT DOMAIN 19 136
 CC FT DOMAIN 146 229
 CC FT DOMAIN 236 330
 CC FT SITE 518 523
 CC FT SITE 542 547
 CC FT DISULFID 36 170
 CC FT DISULFID 41 101
 CC FT DISULFID 164 213
 CC FT DISULFID 269 314
 CC FT CARBOHYD 100 100
 CC FT CARBOHYD 210 210
 CC FT CARBOHYD 231 231
 CC FT CARBOHYD 253 253
 CC FT CARBOHYD 328 328
 CC FT CARBOHYD 375 375
 CC FT CARBOHYD 384 384
 CC FT CARBOHYD 393 393
 CC FT VARIANT 72 72
 CC FT VARIANT 215 215
 CC FT VARIANT 322 322
 CC FT CONFLICT 309 309
 CC FT CONFLICT 358 358
 CC FT CONFLICT 388 388
 CC FT CONFLICT 403 403
 CC FT CONFLICT 403 403
 CC M -> V (in dbSNP:1807124).
 CC F -> S (in dbSNP:2278831).
 CC /FTID=VAR_014251.
 CC E -> K (in REF. 1).
 CC R -> W (in REF. 1).
 CC A -> P (in REF. 1).
 CC S -> N (in REF. 1).

SQ SEQUENCE 551 AA; 60715 MW; 2FEA2B6B341EFAF CRC64;
 Query Match 29.7%; Score 804.5; DB 1; Length 551;
 Best Local Similarity 33.8%; Pred. No. 3.3e-49;
 Matches 206; Conservative 70; Mismatches 172; Indels 161; Gaps 11;

QY 2 LPLPLLSLL-GGSQAMDRGFMIKRVQESVWVWPEGLCISVPCSFSPYPRODTGTPAYGYW 60
 Db 1 MLPLLLPLLMGSLGDEKPYELQVQKSVYVQGLCVLVCSFSYPMRSMYSPLLYVW 60
 QY 61 FRAVTTTGAPATVTHQSEVEMSTRGRQLTGDPKAGCSLYVDAQMODSOFYFRV 120
 Db 61 FRCGEIPVYAEVATNNPRKVPETQGRFLGDVQKKCSISIGARMEDGYSYFRV 120
 QY 121 ERGSYRVNPMNDGFLKVTALQKPDVYPTLEPGOPVTVCVFMAEECPPEFSM 180
 Db 121 ERGRDVKYSYQCKKLEVTALKEPDHLEPLESGRPRLCSLPGSEACAPPLTFSM 180
 QY 181 TGAALSSQGTPTTSHFSVLSFTPRQDHDITLCHVDSRKVSQRTVRLVAYAPRD 240
 Db 181 TGNALSP--LDPETTRSSSELTLPREDHGTNLTCQMKRQAGVTTERTVQLNVSAPQT 238
 QY 241 LVYSISRDNTPPDPENLRWVNSQANTVLENLNGSTSLPYLEQSICLVCTVHTSPPARL 300
 Db 239 ITTF-----RNGIALEIILQNTSYLPVLEQALRLCLDAPSNPRAHL 279
 QY 301 SPTQRGVLPSPQSPDPVLELPVQVHEGFEPTCAHAPHLGSOHSLSVHYKKGLIS 360
 Db 280 SMOGSSPALNATPISMTGILRLRVSAEAGGTCAQNHPLGLQIFLNLSVSLPQLLG 339
 QY 361 TAFS----- 364
 Db 340 PSCSWAEGLHCRCSEFRAPAPSLCWRLEEKPLEGNSQGSFKVNSSAGPMANSLILH 399
 QY 365 -----NGAFL-----GIGTALLFLCLALIM 386
 Db 400 GGLSSDLKVCAMWNIYSGSGSVLLQGRSNLTGVPALGAGMALLCICLCIIF 459
 QY 387 KILPKRRQTETPRPFRSHSTILDYINVPYTAGPLAQKRNKATPNSPTPT-PPGAPS 445
 Db 460 LIYKARRKQA-AGRPEKMDDED-----PIMGITSSGRKKPWPDSPPDOASPPEDAP 510
 QY 446 PESKKKKQKQYOLPSPEPKSSQOAPESQSEELHYATLNFQVRRPRAPRMPKQTQA- 504
 Db 511 P-----LEEKELHYASLSFSEMK-----SREPKQDEAP 539
 QY 505 ----DYAEVK 510
 Db 540 STTEYSEIK 548

RESULT 11
 CD33_HUMAN STANDARD: PRT; 364 AA.
 AC P20138; Q8TD24;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Myeloid cell surface antigen CD33 precursor (gp67) (Siglec-3).
 GN CD33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Promonocytic lymphoma;
 RX MEDLINE=89009814; PubMed=3139766;
 RA Simmons D., Seed B.;
 RT "Isolation of a cDNA encoding CD33, a differentiation antigen of
 myeloid progenitor cells.";
 RL J. Immunol. 141:2797-2800(1988).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21940633; PubMed=11943481;
 RA Yousef G.M., Oordon M.H., Fousias G., Diamandis E.P.;
 RT "Genomic organization of the siglec gene locus on chromosome 19q13.4
 and cloning of two new siglec pseudogenes.";
 RL Gene 286:259-270(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Leukocyte;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshilyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huljk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SIALIC ACID BINDING.
 RX MEDLINE=95235021; PubMed=7718872;
 RA Freeman S.D., Kelm S., Barber E.K., Crocker P.R.;
 RT "Characterization of CD33 as a new member of the sialoadhesin family
 of cellular interaction molecules.";
 RL Blood 85:2005-2012(1995).
 RN [5]
 RP FUNCTION. PHOSPHORYLATION OF TYR-340 AND TYR-358, MUTAGENESIS OF
 TYR-358, AND INTERACTION WITH PRPN6.
 RX MEDLINE=20025980; PubMed=10556798;
 RA Uyanova T., Blasoli J., Woodford-Thomas T.A., Thomas M.L.;
 RT "The sialoadhesin CD33 is a myeloid-specific inhibitory receptor.";
 RL Eur. J. Immunol. 29:3440-3449(1999).
 RN [6]
 RP PHOSPHORYLATION OF TYR-340 AND TYR-358, INTERACTION WITH PRPN6 AND
 PTPN11, AND MUTAGENESIS OF TYR-340.
 RX MEDLINE=99223460; PubMed=10206955;
 RA Taylor V.C., Buckley C.D., Douglas M., Cody A.J., Simmons D.L.,
 RA Freeman S.D.;
 RT "The myeloid-specific sialic acid-binding receptor, CD33, associates
 with the protein-tyrosine phosphatases, SHP-1 and SHP-2.";
 RL J. Biol. Chem. 274:11505-11512(1999).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=21244678; PubMed=11320212;
 RA Vitale C., Romagnani C., Puccetti A., Olive D., Costello R.,
 RA Chiosso L., Pitto A., Baccigalupo A., Moretta L., Mingari M.C.;
 RT "Surface expression and function of p75/ATR-1 or CD33 in acute
 myeloid leukemias: engagement of CD33 induces apoptosis of leukemic
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5764-5769(2001).
 CC -!- FUNCTION: Putative adhesion molecule of myelomonocytic-derived
 cells that mediates sialic acid dependent binding to cells.
 CC Preferentially binds to alpha2,6-linked sialic acid. The sialic
 CC acid recognition site may be masked by cis interactions with
 CC sialic acids on the same cell surface. In the immune response, may
 CC act as an inhibitory receptor upon ligand induced tyrosine
 CC phosphorylation by recruiting cytoplasmic phosphatase(s) via their
 CC SH2 domain(s) that block signal transduction through
 CC dephosphorylation of signaling molecules. Induces apoptosis in
 CC acute myeloid leukemia (in vitro).
 CC -!- SUBUNIT: Interacts with PRPN6/SHP-1 and PTPN11/SHP-2 upon

phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Monocytic/myeloid lineage cells.
 CC -1- DOMAIN: Contains two copies of an intracytoplasmic motif referred
 CC as immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 CC motif is involved in downmodulation of cellular functions as the
 CC termination of the immune response. The phosphorylated ITIM motif
 CC binds to the SH2 domain of PTPN6/SHP-1 and/or PTPN11/SHP-2.
 CC -1- PTM: Phosphorylated on tyrosine residues.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
 CC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- DATABASE: NAME-PROV; NOME-CD guide CD33 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/ncbi/ncbi/ncbi.htm".
 CC -----
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 CC -----
 DR EMBL: M23197; AAA51948.1; ALT_SEQ.
 DR EMBL: AY040541; AAK83654.1; -.
 DR EMBL: BC028152; AAK28152.1; -.
 DR PIR: A30521; A30521.
 DR HSSP: Q62230; IOFO.
 DR Genev: HGNC:1659; CD33.
 DR MIM: 159590; -.
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0004872; F: receptor activity; TAS.
 DR GO: GO:0007267; P: cell-cell signaling; TAS.
 DR GO: GO:0008285; P: negative regulation of cell proliferation; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; Ig; 2.
 DR PROSITE: PS50835; IG-LIKE; 2.
 DR Cell adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein;
 KW Phosphorylation; Immunoglobulin domain; Repeat; Multigene family.
 FT SIGNAL 1 17
 FT CHAIN 18 364
 FT DOMAIN 18 359
 FT TRANSMEM 260 282
 FT DOMAIN 283 364
 FT DOMAIN 19 135
 FT DOMAIN 145 228
 FT SITE 338 343
 FT SITE 356 361
 FT DISULFID 36 169
 FT DISULFID 41 101
 FT MOD_RES 163 212
 FT MOD_RES 340 340
 FT MOD_RES 358 358
 FT CARBOHYD 100 100
 FT CARBOHYD 113 113
 FT CARBOHYD 160 160
 FT CARBOHYD 209 209
 FT CARBOHYD 230 230
 FT MUTAGEN 340 340
 FT MUTAGEN 358 358
 FT CONFLICT 69 69
 FT SEQUENCE 364 AA; 39726 MW; 1973E196940FB16F CRC64;
 Query Match 25.68; Score 694; DB 1; Length 364;

Best Local Similarity 32.8%; Pred. No. 1,1e-41;
 Matches 168; Conservative 59; Mismatches 137; Indels 148; Gaps 8;
 QY 1 MLPLLLSLGSGQAMDRFMTIRVOESWVBEGLCTSPGCFSTPRDWTGSTPAYGW 60
 Db 1 MLPLLLPLLMGALAMDENFWLQVSEYVBEGLCVPCFEPFPIPYDKNSVHWXW 60
 QY 61 FAVETTTGAPVATNHOSEVEMSTGRFQLTGPDKNGSLVRDQOMODESQYFRV 120
 Db 61 FREGALISDSDPVANKNKIDQVEYEGTQGRFLGPPSRNCSLSYDARRRNGSYFRM 120
 QY 121 EGGSVRYRPMNDGFFLKVTALTQKPDVYIPETLEPGQPVYICVFNMAFECPPSPSW 180
 Db 121 EGGV--TKSYSKSPQSLSVHTDITLTPKILIPETLEPGHKNLTCSVSNACQGPPIPSW 179
 QY 181 TGAALSQGTKPTTSHFSVLTSPRPOHDITLCHVDYFSGKYSAGQRTVLRVAYARD 240
 Db 180 LSAAPTSLG--PRTHSSVLTTPRQDHGNTLTCQVFAAGVTTERTIOLANTVYVQN 237
 QY 241 LVISISRDNDPPEPNLRVMVSOANRVTLENIGNSTSLPVLGQSLICVTVTHSSPARL 300
 Db 238 PTTGIFP-----GDG----- 247
 QY 301 SMTQGVLTSPSQSDPGVLELPRQVHEGEFTCHARHPLGSOHVSLSVHYKGLIS 360
 Db 248 -----SGKQETRAGV----- 258
 QY 361 TAFNSGAFVIGITATLFLCALIIMKILPRRTQTEPRPRFSRSTIIDYINVPTAG 420
 Db 259 ---HGAIGAGVATALLALCLIFLYKTHRRKAARTAVGRNDH-----PTTG 304
 QY 421 PLAKRNQKATPNPSPRPLPGAPSPESKKNQKQYOLPSPPEKRSQAPESQSEQL 480
 Db 305 SASRHKQKSLHGP-----TETSSGCAAPVEMDEEL 338
 QY 481 HYATLNPVYPRPEARMKPGTQADVAEVKQ 512
 Db 339 HYASLNFHGMNP-----SKDTREYSEVARTQ 364
 RESULT 12
 SILE_MOUSE STANDARD; PRT; 569 AA.
 ID SILE_MOUSE
 AC Q920G3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Sialic acid binding Ig-like lectin-F precursor (mSiglec-F).
 GN SIGLEC-F.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=21576254; PubMed=11579105;
 RA Angata T., Hingorani R., Varki N.M., Varki A.;
 RT Cloning and characterization of a novel mouse Siglec-F;
 RT differential evolution of the mouse and human (CD33) Siglec-3-related
 RT gene clusters.;
 RL J. Biol. Chem. 276:45128-45136(2001).
 CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,3-
 CC linked sialic acid. The sialic acid recognition site may be masked
 CC by cis interactions with sialic acids on the same cell surface.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed by immature
 CC monocytic/myeloid lineage cells in bone marrow. Also found at
 CC lower levels in mature neutrophils and monocytes.
 CC -1- DOMAIN: Contains an intracytoplasmic motif referred as
 CC immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif
 CC is involved in downmodulation of cellular functions as the


```

DB      10 FMIMISASRGHGMAMPSSISAEFGTCSICRFEDFP--DELRAVAVGVYFNSPYPK 67
OY      69 KCAPATNHQSHREVMSTRGRFQLTGDPKAGNCSLVINDAQODESQVFRFRERSYAK 128
DB      68 NVPFVKSRIQOVHESFQGRSRLGDLGRNCTLLLSVSPSELGKYYFRDGLGYNQY 127
OY      129 NFMNDGFLKYATLQKPDVYIPETLEPQPVTVICVFNMAEECP--PSSMTG---- 182
DB      128 TFSFH-----SVLDIYNTNRIYVPRVAVGTEVEGCMF--DNCEPLRELSWIGHHEL 180
OY      183 ---AALSS-QGTRKPTTSHFSVLSFTPRQDHDITLCHVDFSRKVSQAQRTVRLRAYAP 238
DB      181 GEPALVGLRDEGTGWQVSLHFVPTREANGHRLGCGASFPNTILOFGYASMDVKKYP 240
OY      239 RDLVISIS-----RDNTPPD-----PENLRVMY----- 261
DB      241 VIVEMNSSVEALEGSHVSLLCGADSNPPPLLTMMRDGTVLREAVAESLLELEEVTPAED 300
OY      262 -----SQANRTV-----LENLNGTSLPVLEGQSLCVCTHSSPPARLSM 302
DB      301 GYVACLAEANVQDNRITGLSVYAPKPTVNGTVAV--EGETVSLICSTQSNPDIILTI 359
OY      303 TORGVLSPPSPDGVLELPRVQVEHEGEFTCHARHPLGSGHVSLSLVHYKKGIL--- 359
DB      360 FKEKQILSTVIESELELPAVSPEDDEGYCVAENQGORATAPNLISVEFAPVLLLES 419
OY      360 -----STAR-----SNGAFL-----GIGTALLFLCIA 382
DB      420 HCAAADRVOCICVYKSNPEPSVAFELPSRNVTVESEREFEVYSERSGLVLSLTL--- 476
OY      383 LITMILPKRRTOTEMP-----RPRFSRHSITLDY-----INVPTAGPLA---- 423
DB      477 -----KQQAQAPPRVITCTANRLVGAKSLELPQCAHMLMAKTIPTVAVYAFAIL 526
OY      424 -----OKRNOKATPNSPRTPLP-----GAFSP-ESKKNOKKOYOLPSF 461
DB      527 IAIVCYITQTRKKKNVTSPFSAGDNPPVLFSSDFRISGAEKEKESERLGL 586
OY      462 PEPKSTQAPESQESQELHYATLNFPCYRPPREARMRGTOADAEVK 510
DB      567 -----RGEPELLDLSYSHDL-GKRPKDSYTLTEELAEYAEIR 624

RESULT 15
SMP_COTUA STANDARD; PRT; 620 AA.
AC 092154;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Schwann cell myelin protein precursor (Siglec-4b).
GN CN
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosaustra; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OY NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-28; 120-132; 135-157 AND
RP 563-571.
RX MEDLINE=92153423; PubMed=1739462;
RA Dulac C., Tropek M.B., Cameron-Curry P., Rossier J., Marshak D.R.,
RA Roder J., Je Douratin N.M.;
RT "Molecular characterization of the Schwann cell myelin protein, SMP;
RT structural similarities within the Immunoglobulin superfamily.";
RL Neuron 8:333-334(1992).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Exclusively expressed by myelinating and
CC nonmyelinating schwann cells and oligodendrocytes.
CC -1- DEVELOPMENTAL STAGE: First synthesized at embryonic day 5, 1t
CC remains expressed by cultured Schwann cells.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC

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CC      CC      (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
CC      CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      CC      -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC      CC      -----
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      CC      the European Bioinformatics Institute. There are no restrictions on its
CC      CC      use by non-profit institutions as long as its content is in no way
CC      CC      modified and this statement is not removed. Usage by and for commercial
CC      CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      CC      or send an email to license@isb-sib.ch).
CC      CC      -----
CC      CC      EMBL: S83711; AAB21466.1; -.
CC      CC      DR PIR: JH0593; JH0593.
CC      CC      DR HSP: P56276; ITIK.
CC      CC      DR InterPro: IPR007110; Ig-like.
CC      CC      DR InterPro: IPR003598; Ig_C2.
CC      CC      DR InterPro: IPR003006; Ig_MHC.
CC      CC      DR Pfam: PF00047; Ig_2.
CC      CC      DR SMART: SM00408; Igc2; 2.
CC      CC      DR PROSITE: PS50835; IG_LIKE; 2.
CC      CC      KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
CC      CC      Immunoglobulin domain; Repeat.
CC      CC      FT CHAIN 1 17
CC      CC      FT SIGNAL 1 17
CC      CC      FT CHAIN 18 620
CC      CC      FT DOMAIN 18 516
CC      CC      FT TRANSMEM 517 536
CC      CC      FT DOMAIN 537 620
CC      CC      FT DOMAIN 28 106
CC      CC      FT DOMAIN 151 233
CC      CC      FT DOMAIN 239 322
CC      CC      FT DOMAIN 325 407
CC      CC      FT DOMAIN 414 485
CC      CC      FT DOMAIN 35 164
CC      CC      FT DISULFID 40 99
CC      CC      FT DISULFID 158 216
CC      CC      FT DISULFID 260 304
CC      CC      FT DISULFID 346 391
CC      CC      FT DISULFID 420 429
CC      CC      FT DISULFID 431 488
CC      CC      FT CARBOHYD 222 222
CC      CC      FT CARBOHYD 314 314
CC      CC      FT CARBOHYD 331 331
CC      CC      FT CARBOHYD 405 405
CC      CC      FT CARBOHYD 449 449
CC      CC      FT SEQUENCE 620 AA; 66943 MW; 004B3EC7EBC18FBA CRC64;
CC      CC      Query Match 11.2%; Score 302.5; DB 1; Length 620;
CC      CC      Best Local Similarity 22.4%; Pred. No. 6,6e-14;
CC      CC      Matches 148; Conservative 89; Mismatches 224; Indels 199; Gaps 29;
OY      5 LLLSLIGSQAMDGFMRVQESVAVPPGLICISVCSFSYRQDMTGSTPAY--GYWPK 62
DB      4 LVLTVLIMGTGICISAPMAAMPKMAALSGTCVOQLCRPDYDEE---LRPASIGLW- 58
OY      63 AVTEETKCAP-----VATNHQSHREVMSTRGRFQLTGDPKAGNCSLVINDAQODE- 113
DB      59 -----FGSPYKNTNRYPPVYARSPSSAVIHESFAGRASFLGDPGRCTLINI--ARLSEEL 110
OY      114 -SOYFFRVERGSGVRYNFMNDGFLKYATLQKPDVYIPETLEPQPVTVICVFNMAFEE 172
DB      111 ACKYYFRLDGLGYNQSF--SEHAELDYMA---APHLEVHELIVAGSEAEILCRV- 163
OY      173 CPP--PFSFWTGA--ALSSQGR-----PTTSHFSVLSFTPRQDHDITLCHVDFSRK 222
DB      164 CPEPLRLMLWTGTEELDPIGKERLEDLGSLSGLSLFRPKKEDLGRVVGCVFIINS 223
OY      223 GVSAGRTVRLRAYAPR-----DLVISISRDNP-----DP 253
DB      224 SISFADVGLDIDYQERQVVGGLGPTFVVGSGDELGCAGRAPLISFRGSEVAREEP 283
OY      254 PENLRVMSQAN-----RTYLEN-----LGNGTSLPVLEGQSL 286

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Db      284 GRNRLILSNVGPDDGGSFSCVAENNRHNRSLQLRAVAPRAPHYING-SLMVVSQDPV 342
QY      287 CLVCYTHSSPPARLSWTORGOVILSPSQSPDPGVLELPRVQVEHEGEFTCHARHPLGSGHV 346
      : | | | | : | | : | | : | | : | | : | | : | | : | |
Db      343 SVTCRAESEPAIILVLRGKVMAMAIYDHYTMEKRRPARPEDGTTSCVAENOHGASST 402
QY      347 SLSLSVHYKKGLI-----STAF----- 363
      | : | | | : |
Db      403 SFNISVEYPPILVPASRCTAGSDGVRCVMVNSIPDSSLVFELEPTRNQTVSDGHRDFTAA 462
QY      364 ---SNGAFLEIGIT-----ALLFLCLALITMKILPKRRYOTETPRPRFSRH----- 406
      | : | | | : | | | | : | | : | | : | |
Db      463 PPGSDGSTITGL-LTLRGPLEPRLVLCA-----RNRHGTARQLRFHHPGGLVMAK 513
QY      407 ---STILDYINVPPTAGPLAQKRNQKATPNSPRTPLPP-----GAPSPESKKNQ----- 452
      : : | | : | | : | | : | | : | | : | | : | |
Db      514 VGPVGAVVAFAIVAVCVLGSRRKKAGSPETVPQPMAGPGGDDPDLDLRPOQVYRMLR 573
QY      453 ---KKQYQLPSFPPEPKSSTQAPESQESQELHYATLNFPGVRRPEARMKGTQADYAEVK 510
      : : | | : | | : | | : | | : | | : | | : | |
Db      574 GAMERWAL-----GVKEGSGAP--QEVPTPSH-----PPMKP--TRGPLEDDPEYAEIR 618
```

Search completed: October 8, 2003, 20:03:37
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2003, 17:25:21 : Search time 64 Seconds
(without alignments)
2064.421 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLLSLGLGSQLAMDGR.....RPEARMPKCTQADYAEVKRQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1211.5	44.8	623	11	Q8BY18	Q8by18 mus musculu
2	909	33.6	568	4	Q81YH7	Q81yh7 homo sapien
3	664	26.9	11	Q8BTG2	Q8btg2 mus musculu	
4	530.5	19.6	304	4	Q81W38	Q81w38 homo sapien
5	471.5	17.4	423	11	Q8BU57	Q8bu57 mus musculu
6	371.5	13.7	287	4	Q9POF8	Q9pof8 homo sapien
7	360.5	13.3	269	6	Q95KP9	Q95kp9 gorilla gor
8	358.5	13.2	271	6	Q95KQ0	Q95kq0 pan paniscu
9	351.5	13.0	269	6	Q95KP8	Q95kp8 pongo pygma
10	235.5	8.7	312	6	Q95JN1	Q95jn1 macaca fasc
11	205	7.6	430	4	Q15600	Q15600 homo sapien
12	198.5	7.3	367	11	Q9PD4M0	Q9pd4m0 mus musculu
13	195.5	7.2	461	4	Q13854	Q13854 homo sapien
14	194.5	7.2	461	4	Q60430	Q60430 homo sapien
15	186.5	6.9	508	11	Q8R007	Q8r007 mus musculu
16	186.5	6.9	508	11	Q8CED8	Q8ced8 mus musculu

17	184	6.8	402	11	Q35444	Q35444 mus musculu
18	183	6.8	483	11	Q9DBP8	Q9DBP8 mus musculu
19	182.5	6.7	577	11	Q9DZ21	Q9DZ21 mus musculu
20	177	6.5	510	4	Q96NY8	Q96NY8 homo sapien
21	175.5	6.5	1252	11	Q9J1X2	Q9J1X2 rattus norv
22	175	6.5	510	4	Q96K15	Q96K15 homo sapien
23	175	6.5	662	4	Q60926	Q60926 homo sapien
24	167	6.2	464	4	Q16170	Q16170 homo sapien
25	167	6.2	468	4	Q96CA7	Q96CA7 homo sapien
26	166.5	6.2	718	5	Q21139	Q21139 caenorhabd1
27	166.5	6.2	1332	5	Q9BN17	Q9BN17 drosophila
28	166.5	6.2	1332	5	Q9VOM7	Q9VOM7 drosophila
29	161.5	6.0	1256	11	Q925S5	Q925S5 mus musculu
30	161.5	6.0	1256	11	Q9J1X1	Q9J1X1 mus musculu
31	161.5	6.0	1256	11	Q9ET59	Q9ET59 mus musculu
32	161	5.9	412	6	Q8H714	Q8H714 oryctolagus
33	159	5.9	650	6	Q9GKR2	Q9GKR2 bos taurus
34	159	5.9	739	6	Q28260	Q28260 canis fam1
35	159	5.9	739	6	Q9GKR3	Q9GKR3 bos taurus
36	155	5.7	213	4	Q8MW91	Q8MW91 homo sapien
37	155	5.7	335	4	Q8TCD9	Q8TCD9 homo sapien
38	155	5.7	1041	4	Q94856	Q94856 homo sapien
39	155	5.7	1217	11	P97685	P97685 rattus norv
40	153.5	5.7	494	11	Q9ESC6	Q9ESC6 mus musculu
41	153	5.7	5636	4	Q96RW7	Q96RW7 homo sapien
42	152.5	5.6	373	4	Q9H6B4	Q9H6B4 homo sapien
43	152	5.6	467	4	Q8NR8	Q8NR8 homo sapien
44	151.5	5.6	1151	11	Q9QVN5	Q9QVN5 rattus sp.
45	151.5	5.6	1174	11	Q91260	Q91260 rattus norv

ALIGNMENTS

RESULT 1	ID	Q8BY18	PRELIMINARY;	PRT;	623 AA.
AC	Q8BY18				
DT	01-MAR-2003 (TREMBLrel. 23, Created)				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	Weakly similar to stailic acid-binding lectin (Fragmen).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-C57BL/6J; TISSUE=Thymus;				
RX	MEDLINE=22354683; PubMed=12466851;				
RA	THE FANTOM Consortium				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs."				
RL	Nature 420:563-573(2002).				
DR	EMBL: AK042488; BAC31272.1; -				
FT	NON_TER	623	623		
SQ	SEQUENCE	623 AA;	63384 MW;	5827C09D52C3AC7F	CRC64;
Query Match		44.8%;	Score 1211.5;	DB 11;	Length 623;
Best Local Similarity		43.1%;	Pred. No. 1.3e-96;		
Matches	267;	Conservative	55;	Mismatches	111;
				Indels	187;
				Gaps	8;
QY	2	LLPLLSLGLGSQLAMDGRFWIVQESVWPBGLCTISVPCSFSPRODWTGSPANGYWF	61		
DB	3	LLPLLSLGLDGPQGMESYFLQVORIVYKQDELCTIFVPCSFSPBEGKMNRLSLYGYWF	62		
QY	62	KATVETTKGAPVATFNHOSREVEKSTGRFQDLPKAGNCSTVIRPQAMQDEQYPRVE	121		
DB	63	KGTRKPSLSFPAVTNNKDKLEWBAKRFQDLDISKNCSTLIKDWQMDSTNYPRME	122		
QY	122	RGSYVRYNFMDGFLLKVTALTKQPDVYIETLEPGQPVYVICVFNNAPEECPPSPFSWT	181		

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Db 123 RG-FERESKEE-FRLQVEALTKQPDIFIEVLEPEGPVTVCLFSWTFNQCAPSFSNM 180
QY 182 GAALSSOGKPTTSHFSVLEFTRPDHDTLCHVDFSKGVSAQRTVRLVAAPRDI 241
Db 181 GDAVSFOESRPHSNTSVLSFTIPGLQHDHTELTQDLFSR--MSTQRTVRLVAAPRDI 238
QY 242 VISISBDN--TRP----- 252
Db 239 AISIFHDNVSVPDLHENPHEVQOGQSLRLCTADSOPTATLSWLEQVLSWSSPVGS 298
QY 253 -----PENLRVMSQANKTVLENIG 273
Db 299 FRLALELPVYKADSGHYTQCAENRLGSOQHTLDLSVLPQDLRVTVSQANKTVLELIR 358
QY 274 NGTSLPVEGOSLCTVCTHSSPPARTSWTQGVLSPPSPDPTLPRQVEHEGEF 333
Db 359 NAIISLPVEGOSLCTVCTHSSPPARTSWTQGVLSPPSPDPTLPRQVEHEGEF 418
QY 334 TCHARRPLGSQVHVSLSLVHY-----KKGL----- 358
Db 419 TCAQNPGLGAORISLSLVHYPPQMSPPSCSWEAGLHONCSSRAMPAASLWRLEGL 478
QY 359 -----IS 360
Db 479 EGNSSNASTVTFSSIGPVWVNSSLLDELGPJLWLSCESWNTGAGQTTSVLLPDKDSA 538
QY 361 TAFSNGAFLGIGITALFLCALIIMKILPKRRQTEPRPRFSHTLIDYINVPK 420
Db 539 TAFSGAVLVGFTITLMLACLIVKTLQKGTQEEPSRPLKSLGSLTLDYINVPKTR 598
QY 421 PLAKRNOKATPNSRTPRP 440
Db 599 SLA--RNWKAEPDAPSRSP 616

RESULT 2
Q81YH7 PRELIMINARY; PRT; 568 AA.
AC Q81YH7:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE SIGLEC-like 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI TaxID=9606;
RN RP
RP TISSUE=Blood;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035809; AAH35809.1; -.
SQ SEQUENCE 568 AA; 61977 MW; C955F4D62162B860 CRC64;

Query Match 33.6%; Score 909; DB 4; Length 568;
Best Local Similarity 43.1%; Pred. No. 2,3e-70;
Matches 211; Conservative 65; Mismatches 174; Indels 40; Gaps 10;

QY 7 LSLILGSGQANDGRFWIVQSVWVPEGLCISVPCSFSPRODWTGSTPAYGYWFKVTE 66
Db 110 LSVWVTSQDILSRYLEVESVTVQGLCVSPCSVLVHYHNTASSPVYGSNFKGAD 169
QY 67 TTGCAPVATNHQSEVEMSTRGRFQLTGDPKAGCSLIVDAQMODSQQYFFRVERGSYV 126
Db 170 IPMDIPVATNTPSGKVEDTHGRFLGDPQTNWCSLISIDARKGDSGKYFFQVERGSR- 228
QY 127 RYFMNDGFILKVTALQKPDVYIPETLEPGQPVTVICVNNAFEECPSPFSMTGAALS 186
Db 229 KMYIYDKLSVHTALHMTPTSGTLESGBHPRNLTCVPMACEQGTPTITWMAASVS 288
QY 187 SGTGKPTTSHFSVLEFTRPDHDTLCHVDFSKGVSAQRTVRLVAAPRDIYISIS 246
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Db 289 S--LDEPTTRSSMLSLIPQPDHGTSLTCQVTLPGAGVYTMRAVRLNISY----- 336
QY 247 RNDTDPPENLRVMSQANKTVLENIGNTSLPVEGOSLCTVCTHSSPPARTSWTQRG 306
Db 337 -----PQGNLMTVTFQGDGTASTLRNLSALSVLEGOSLHLYCAVDSNPAPRSLWGS 390
QY 307 QVLSFQSDPGEVLELPRVQVEHEGEFTCHARRPLGSGQVHVSLSLVHYK--KGLISPAF 363
Db 391 LILSPQSSNGLVLELPRVHYVDEGEFTCAQNPPLGSHISLSLQNEYTKMRPISGV 450
QY 364 SNGAFLGIGITALFLCALIIMKILPKRRQTEPRPRFSHTLIDYINWY--PAG 420
Db 451 TIGARGGAGATALVFLYCTILFVVY--RSCRKKSARPAVGQDGMEDANAARVGSASOG 507
QY 421 PLAKRNOKATPNSRTPRP--GAPSESKKNOKQVQLPSPEPKSSTQAPESQOE 478
Db 508 PLI-----BSPADDSPPHNAPALATPSP-----EGELQVYASLSFHKARAPYPOQER-I 557
QY 479 ELHATLWFP 488
Db 558 GYEYSEINIP 567
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RESULT 3
Q8BTG2 PRELIMINARY; PRT; 269 AA.
AC Q8BTG2:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Weakly similar to stalle acid-binding lectin.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
RN RP
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Bone;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK036698; BAC29538.1; -.
SQ SEQUENCE 269 AA; 30882 MW; D2D03B384BDA33C5 CRC64;

Query Match 24.5%; Score 664; DB 11; Length 269;
Best Local Similarity 55.1%; Pred. No. 1,7e-49;
Matches 129; Conservative 36; Mismatches 65; Indels 4; Gaps 3;

QY 2 LILFLLSLILGSGQANDGRFWIVQSVWVPEGLCISVPCSFSPRODWTGSTPAYGYWF 61
Db 3 LILFLFLSLDGGQGMESVYLQVRIVAQOELCTFVPCSFSPGKMLNSPLTYGYWF 62
QY 62 KAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGCSLIVDAQMODSQQYFFRVER 121
Db 63 KGIKRSLSIPVATNKKQVLEWARGRQPLGDISKKCSLIRKQVQMGSDTNFFRME 122
QY 122 RGSYVRYFMNDGFILKVTALQKPDVYIPETLEPGQPVTVICVNNAFEECPSPFSMT 181
Db 123 RG-FERESKEE-FRLQVEALTKQPDIFIEVLEPEGPVTVCLFSWTFNQCAPSFSNM 180
QY 182 GAALSSOGKPTTSHFSVLEFTRPDHDTLCHVDFSKGVSAQRTVRLVAAPRDIYISIS 246
Db 181 GDAVSFOESRPHSNTSVLSFTIPGLQHDHTELTQDLFSR--MSTQRTVRLVAAPRDI 232

RESULT 4
Q81W38 PRELIMINARY; PRT; 304 AA.
AC Q81W38:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
```

DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to CD33 antigen (9p67) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RP TISSUE=Blood;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041072; AAH41072.1; -.
FT NON_TER 1
SQ SEQUENCE 304 AA; 33416 MW; A21DF49DAC3B85B CRC64;

Query Match 19.6%; Score 530.5; DB 4; Length 304;
Best Local Similarity 42.6%; Pred. No. 8e-38;
Matches 110; Conservative 36; Mismatches 87; Indels 25; Gaps 3;

QY 1 MLPLLLSS-----LLGSGQAMDGRFMIVQSSVMVPEGLCTS 38
DB 4 MLPLPLFSANHGSPGSLCRDAAAAAAPAVGRALADARFLMPESVTVQEGLCIF 63
QY 39 VPCSESPRODWTGSTPAYGWFKAVTETTKGAPVATNHQSEVENSTGRFQLTGDPAK 98
DB 64 VHCSEVYLEYGMNDSTPAYGHWFRGVSVDQETPVTNNTSTOKVQKGTGRFHLDDPSR 123
QY 99 GNCSLVIRDAOMODESQYFFRVERGVSRYRNFEMNDGFLKVTALTKOPDVYIPELPEGO 158
DB 124 NNCSTLSIRDAARRDNCSYFFVWAAGR-TKFSYKSPSLSYVATLTHRPDLILPEFLKSGH 182
QY 159 PTYVICFVMAFEECPSPFSMTGALSSQGTPTSHFSYFTRPDHDDTLCHVD 218
DB 183 PSNLTCSYVWCEGQTPPIFSWMSAAPTSLG--PRLHSSVLTIIIPQDGTNLICQVT 240
QY 219 FSRKGVSAQRTVRLRAY 236
DB 241 FPGAGVTERTIQLSYSW 258

RESULT 5

Q8BU57 PRELIMINARY: PRT; 423 AA.
AC 08BU57;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Static acid-binding lectin SIGLEC-F homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=22354683; Pubmed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK087658; BAC39955.1; -.
SQ SEQUENCE 423 AA; 45208 MW; 7393D0E4BE5BFA55 CRC64;

Query Match 17.4%; Score 471.5; DB 11; Length 423;
Best Local Similarity 29.3%; Pred. No. 1.7e-32;
Matches 134; Conservative 59; Mismatches 117; Indels 147; Gaps 12;

QY 100 NCSLVIRDAOMODESQYFFRVERGVSRYRNFEMNDGFLKVTALTKOPDVYIPELPEGO 159
DB 8 NCSLDIRDAOKIDTGYFFRLD-GS-VKYSFQKSMLSLVIALTEVPNIQVSTLVSGNS 65

QY 160 VTIVICVFNMAFEECPSPFSMTGALSSQGTPTSHFSYVLSFTPRPDHDDTLCHVD 219
DB 66 TKILCSVPNACEGTPTPIFSWMSALTSLSGHTTSL--SLNLTTPRODGTNLICQVNL 123
QY 220 SRKGVSAQRTVRLRAYAPRDLYISIRNDTPPPENLRVMSQANRTVLNGLNGLSLP 279
DB 124 PGGVYVERTOQLSLVIA-----PQKMTIRVSMGDDTGKVLQSGASLQ 167
QY 280 VLEGSGLCIVCYVHSSPARLSWTQRCQVLSPPSPDPVGLTLPVQVHEHGEFTCARH 339
DB 168 IQEGESLIVCMKDSNPVAVLSWERPTQ--KPPQLSTPAELQLPRALEDOQKRTICQAO 225
QY 340 PLGSOHVSLSLSV-----HYKKG----- 357
DB 226 SQGAQNASVLSIRSLVOLLGSPCSFEGGLHSCSSRAMAPASLRRLRGLGVLGNSN 285
QY 358 -----LISTAPSN----- 365
DB 286 GSFTVKSASAGQWANSLSLISMEFSSNHLRSCAWSDNRVQATLILVSGPKVSOAGKSE 345
QY 366 -----GALIGIGTALLFLCLALIT--KKILPKRTQETPRPRPSRSTLIDYINV 416
DB 346 TSRGTVLGAITGALMALAVCLCLIFETVKVLRKNSA-----LKVA 387
QY 417 PTAGPLAQKRNQKATPNS--PTPLPPGAPSPESKK 450
DB 388 ATKGNHLAK-NPASTINSASITSSNTALGTFPMGOSSE 423

RESULT 6

Q9POF8 PRELIMINARY: PRT; 287 AA.
AC 09POF8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE HSPC078 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RP TISSUE=Umbilical cord blood;
RA Zhang Q.H., Ye M., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Ran H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT Human partial CDS cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161341; AAF28901.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 287 AA; 31664 MW; 85F36EBB6C5C1C11 CRC64;

Query Match 13.7%; Score 371.5; DB 4; Length 287;
Best Local Similarity 44.3%; Pred. No. 4.9e-24;
Matches 74; Conservative 30; Mismatches 60; Indels 3; Gaps 2;

QY 70 GAVPATNHQSEVENSTGRFQLTGDPKACNSLVIRDAOMODESQYFFRVERGVSRYRN 129
DB 72 GDSMATNNTSTOKQKEQKGFHLGDPSSRNKCSLTDARRDNQSTFFVYAR-RRTKFS 130
QY 130 FNMDFELKVTALTKOPDVYIPELPEGOPTVIVCNMAFEECPSPFSMTGALSSG 189
DB 131 KYSPSLSVYTALTTHRPDLILPEFLKSGHSNLTCSVPWCEGCTPIFSWMSAAPTSLG 190
QY 190 TKPPTSHFSVLSFTPRPDHDDTLCHVDSSRKGVSAQRTVRLRAY 236
DB 191 --PRLHSSVLTIIIPRODGTNLICQVTEPGAAGVTERTIQLSYSW 235

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RESULT 7
Q95KP9 PRELIMINARY; PRT; 269 AA.
AC Q95KP9;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Static acid-binding lectin siglec-1l (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_Taxid=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL; AY029755; AAK50563.1; JOINED.
DR EMBL; AY029754; AAK50563.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
DR Lectin.
KW NON_TER
FT
SQ SEQUENCE 269 AA; 30436 MW; 96E49E4F779D6E50 CRC64;

Query Match 13.3%; Score 360.5; DB 6; Length 269;
Best Local Similarity 37.2%; Pred. No. 4.1e-23;
Matches 93; Conservative 41; Mismatches 83; Indels 33; Gaps 11;

QY 1 MLPLLLSLIGSQAMDGRFWIRVOESWVPEGLCTISVPCSFYPRQDWTGSPAYGYW 60
   ||| || : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 LLPLPLCGRGAKGKQD--YLLTMQKSVTVQEGLCVSLCSFSPQMGWTDSDPVHGYW 63
QY 61 FKAIVETTKGAPVATNHNOSREVENSTGRFQLTGDPKAGNSLYIRDAQODESOYFFRV 120
   || : : ||| ||| : : : : : ||| ||| ||| ||| ||| ||| |||
DB 64 FRAGDHVSRYNPVATNPNPRAVQETRDRLDGPQNKDCTLSIRDTRESDACTYVERV 123
QY 121 ERGSYVRNFMNDGFEFLKVT--LTKRPDYIPE--TLEPGQVTVICV-----FNMAF 170
   ||| : : : : : ||| ||| : : : : : ||| ||| ||| ||| ||| |||
DB 124 ERGN-MKWNKYKYYDLSVNTASQDLISRYRLEVESYTVQGLCVSPCSLYRHYNMTA 182
QY 171 EECPPPSFSW--TGAAL-----SSQGTKPTTSHFSVLSFTPRPDHDTLNCVH 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 183 SS--PVYGSWFKEGADIPWDIPVATNTPGKGVQEDTGRFLLG---XPGTNCSLS--I 235
QY 218 DFRKGVSAQ 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 RDARKGDSGK 245

RESULT 8
Q95KCO PRELIMINARY; PRT; 271 AA.
AC Q95KCO;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Static acid-binding lectin siglec-1l (Fragment).
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_Taxid=9597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).

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DR EMBL; AY029753; AAK50562.1; -
DR EMBL; AY029752; AAK50562.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Lectin.
KW NON_TER
FT
SQ SEQUENCE 271 AA; 30613 MW; F63E6018C1CB934 CRC64;

Query Match 13.2%; Score 358.5; DB 6; Length 271;
Best Local Similarity 36.4%; Pred. No. 6.1e-23;
Matches 91; Conservative 42; Mismatches 84; Indels 33; Gaps 10;

QY 1 MLPLLLSLIGSQAMDGRFWIRVOESWVPEGLCTISVPCSFYPRQDWTGSPAYGYW 60
   ||| || : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8 LLPLPLCGRGAKGKQD--YLLTMQKSVTVQEGLCVSLCSFSPQMGWTDSDPVHGYW 65
QY 61 FKAIVETTKGAPVATNHNOSREVENSTGRFQLTGDPKAGNSLYIRDAQODESOYFFRV 120
   || : : ||| ||| : : : : : ||| ||| ||| ||| ||| ||| |||
DB 66 FRAGDHVSRYNPVATNPNPRAVQETRDRLDGPQNKDCTLSIRDTRESDACTYVERV 125
QY 121 ERGSYVRNFMNDGFEFLKVT--LTKRPDYIPE--TLEPGQVTVICV-----FNMAF 170
   ||| : : : : : ||| ||| : : : : : ||| ||| ||| ||| ||| |||
DB 126 ERGN-MKWNKYKYYDLSVNTASQDLISRYRLEVESYTVQGLCVSPCSLYRHYNMTA 184
QY 171 EECPPPSFSW--TGAAL-----SSQGTKPTTSHFSVLSFTPRPDHDTLNCVH 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 SS--PVYGSWFKEGADIPWDIPVATNTPGKGVQEDTGRFLLG---DPTNCSLS--I 237
QY 218 DFRKGVSAQ 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 238 RDARKGDSGK 247

RESULT 9
Q95KP8 PRELIMINARY; PRT; 269 AA.
AC Q95KP8;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Static acid-binding lectin siglec-1l (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
DR EMBL; AY029757; AAK50564.1; -
DR EMBL; AY029756; AAK50564.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Lectin.
KW NON_TER
FT
SQ SEQUENCE 269 AA; 30649 MW; D21277346EC3CTCA CRC64;

Query Match 13.0%; Score 351.5; DB 6; Length 269;
Best Local Similarity 36.0%; Pred. No. 2.5e-22;
Matches 90; Conservative 42; Mismatches 85; Indels 33; Gaps 10;

QY 1 MLPLLLSLIGSQAMDGRFWIRVOESWVPEGLCTISVPCSFYPRQDWTGSPAYGYW 60
   ||| || : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 6 LLLPRLCGVGAKEQD--YLLTMQSVTVQEGLCVSLCSFSYPODDMTSDPYHGWM 63
QY 61 FRAVETETGAPATVATNHSOREVEMSTRGRFOLITGDPKAGNCSTVIRDAQMDQESQYFFR 120
Db 64 FRAGDHVSNILVATNTNPAARAREETRDPRFHLIDPQONKCTSLTSDTRESDAGYFFR 123
QY 121 ERGSYVRNFMNDGFELKYTA--LTQKPDVYIPE--TLEPGQPVTVICV-----FNMAF 170
Db 124 ERGN-1KMSYKHDOQSVNTYASQDLISRYRLEVEPVQEGLCXVPCSVLPHYNMTRA 182
QY 171 EECPPPSFSW--TGAAL-----SSQGTKPTTSHFVSLSFTPRQDHDITLCHV 217
Db 183 SS--PYGSGWFKREGADIXMDIPVATNTPSGKVOEDTQGRFLLG--DPQTNCSLS--I 235
QY 218 DFRKGVSAO 227
Db 236 RDAKKGDSK 245

RESULT 10
095JN1 PRELIMINARY: PRT: 312 AA.
AC 095JN1: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS Hypothetical 34.6 kDa protein.
OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC NCBI_TaxID=9541;
RN [1]
RP TISSUE=Testis;
RC Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA Terao K., Sugano S.;
RT Isolation of novel full-length cDNA clones from macaque testis cDNA
RT libraries.*;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB070150; BAB63095.1; -;
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 34610 MW; 42CA54C314CCLCF0 CRC64;

Query Match 8.7%: Score 235.5; DB 6; Length 312;
Best Local Similarity 24.5%: Pred. NO. 3.6e-12;
Matches 93; Conservative 44; Mismatches 140; Indels 103; Gaps 13;

QY 92 LTGDPKAGNCSTVIRDAQMDQESQYFFRERGSYVRNFMNDGFELKYTALQKPDVYIP 151
Db 1 MGNNDDEEDCTLIHILKNGSNATYLFYADLGEQ-KSAFLGENIKRFLFSDITQKPELHP 59
QY 152 ETLPEGQPVTVICVFENMAFEECPSPFSWTGAALSSQGTKPTTSHFVSLSFTPRQDHD 211
Db 60 ETLLEKPAALNCTLTGCTCKEIKALFRSRKNPAVSS-----SSSVPHFILRPDHCN 112
QY 212 DLTCHVDPSRKGVSAQRTVLRVAAYAPROLVISISDNTPRDPENLRVWVSAQNRVLEN 211
Db 113 TLGCHNFSFLANTNSLVAKLVVSPHRLFNSSCS----- 147
QY 272 LQNGTSLPVLEGOSLCLVCTHSSPARLSWTORGQVLSPOSPDPGLE-LPRV----- 325
Db 148 -----LEKTVLC-SCSFHGIPRPSQVMWNG-----VPDVNMSDNIDPRVYSSNR 191
QY 326 -----QVEHEGEFTCHARRPLDSQHVLSLSVHYKGLISTAFNSAGFLGT-- 371
Db 192 VPMANSTINLIGPEIYMRLRCEGKNQYGI-HTSSFFLLIPNKKS-VSSMFVKLIGIYV 249
QY 372 GITA--LFLCLALILIKIL-----FKRRQTQTPRPRSRHSITIIDYIVVYTAGP 421
Db 250 GAIAISLFLPCLLLMLKMLNMWEEHQSFRTKEGLTKRPELLEPEV----- 297
QY 422 LAQKRNOKATPNSPTPLPP 441

Db 298 -----PSMWEADIPP 307

RESULT 11
015600 PRELIMINARY: PRT: 430 AA.
AC 015600: 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN TM2-CEA precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP TISSUE=Colon adenocarcinoma;
RC MEDLINE=89139550; PubMed=2537311;
RA Barnett T.R., Kreschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA Eling J.J., Kamarc M.E.;
RT "Carcinoembryonic antigens: alternative splicing accounts for the
RT multiple mRNAs that code for novel members of the carcinoembryonic
RT antigen family.";
RL J. Cell Biol. 108:267-276(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.M.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala M., Terry A., Barnes J.,
RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Altix C., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Coefield J., Dhar S., Olsen A.S., Carrano A.V.;
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: X14831; CA32940.1; -;
DR EMBL: AC004785; AAC18435.1; -;
DR InterPro: IPR001589; Actbind_actnln.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000920; Myelin_P0.
DR Pfam: PF00047; Ig_3.
DR PRINTS: PR00213; MYELINP0.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Alternative splicing; Immunoglobulin domain; Signal; Transmembrane.
FT SIGNAL 1 34
FT CHAIN 35 430 POTENTIAL.
SQ SEQUENCE 430 AA; 46910 MW; 195DE9F17D1D1414F CRC64;

Query Match 7.6%: Score 205; DB 4; Length 430;
Best Local Similarity 22.6%: Pred. NO. 2.5e-09;
Matches 124; Conservative 73; Mismatches 174; Indels 178; Gaps 29;

QY 5 LLLSLSSQAMDGFWIRVQESVAVPREGICISVP-----CSFSYPODDMTGSTPAY 57
Db 19 LILASL-----TFMNPPTTAQLTTESMPNVAEGKEVLLVHNLPQO-----LF 63
QY 58 GY-WFAVETTKGAPVATNHSOREVEMSTRGRFOLITGDPKAG-----NCSLVIRDAO 109
Db 64 GYSWYKG--ERYDG-----NRQIVGAIGTQATPPANGRETIYPNASLILQNTY 113
QY 110 MODESQYFFRERGSYVRNFMNDGFELKYTALQKPDVYIPELTLPQGPVTVICVFNMA 169
Db 114 QNDTGTYTQV-----IKSDLVNE-----EATGQFHYI----- 141
QY 170 EECPPPSFSWTGAALSSQGTKPTTSHFVSLSFTPRQDHDITLCHVDFSRKGVSAQRT 229

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Db 142 -PELRPS-----ISSNNSNPVEDKAV-AFTCEPETQDTYTLMINOSLPVSP--- 189
QY 230 VALRYAYAPRL-VISISHPNTDPDENLRVWQANRP--VLENIAGNGLSPVE---- 282
Db 190 -RLQISNGRITLTLSVRNDGPECEIQNPVS-ANSDPEPTLVYGPDTPTTSPSDT 247
QY 283 ----GOSICLVCTHSSPPARLSWTQROVLSPPSPDPGVLELRVQVEHEGEFTCHAR 338
Db 248 YRRPQANLSTSCYAASNPAPQYSWMLNGFQOSTQE-----LFINPITVNNSGSYTCAN 302
QY 339 HPL-GSOHVSLSVHYKKGL-ISTAFSNGAFLG--IGITALLFLCLALLIKTL----- 389
Db 303 NSVTGNCNRTYKTIIVTDNALPQENGSLPGALAGIVGVALLVAL-LVALACFLHEGKT 361
QY 390 ---PARRQTETPRPRFSRHSITLIDYINVPTAGPLAQRKQKATPNSPRTPPLPGASP 446
Db 362 GRASDQDRLTE-HKPSVSNHTQ--DHSN-----DP 388
QY 447 ESKKQKQKQYQLPSPPEKSSQTQAPESQESQELHYATLNPQVAP-RPEARMRK--GTQ 503
Db 389 PKKN-----EVTYSLNFEAQDPTQTSASPLTATE 421
QY 504 ADYAEVKFQ 512
Db 422 IYSEVKKQ 430

RESULT 12
Q9D4M0 PRELIMINARY: PRT: 367 AA.
ID 09D4M0:
AC 09D4M0:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE 4931406B18RIK protein.
GN 4931406B18RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Iawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK016431; BAB30231.1;
DR MGD: MGI:1921304; 4931406B18RIK.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PSS0835; IG_LIKE; 1.
SQ SEQUENCE 367 AA; 40625 MW; 24CANDEA63F47F95 CRC64;
Query Match 7.3%; Score 198.5; DB 11; Length 367;

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Best Local Similarity 23.5%; Pred. No. 7.5e-09;
Matches 102; Conservative 65; Mismatches 146; Indels 121; Gaps 22;
QY 1 MLPL-LTSLGSGQADGCRFWIRVOESVWVPGCLTSPCSFYPRQDWTGSTPAYCY 59
Db 9 LLLYLGLISPLV-----VDYKKTAM-EDGLCSMVCVIEF----- 42
QY 60 WEKAVETTKGAPVATNHSREVEKSTGRFLQGDPA--KGNCSLVIRDAQMODESQYE 117
Db 43 -YKAPFRN-----PAVSTRLE-NISFVVG---ISHSAPMGDLS-----TEEVEYC 85
QY 118 FRVERGSYVRYNEMNDGEFLKVTY--LTQRPDYIPELTLPQGPVTVICVFNNAFECR 174
Db 86 ILMTN-SMLRRKRYMNSLYVLGTLQKDLQNPDELHPESSVAGEPVLTSLCTIGSTCEPN 144
QY 175 PPSFSGMGAASQGT---KPTTHFVSLSTPRPDHDTLPCHVDPSKRGVNAQTVR 231
Db 145 ALFTSMKQPIKMSNTTTSIHPS---SALATELKPEDQGTTLRCHLKLSTLDNLSKRYVK 200
QY 232 LRVAAPRDVVISISRDNTDPDENLRVWQANRTVLENIGNGLSLPVEGOSICLVCV 291
Db 201 LQVSPTRFLNYS-----CLIKRTLPGSCS 225
QY 292 THSSPPARLSWTQROVLSPPSPDPGVLELRVQVEHEGEFTCHARPLGSGHVSLSL 350
Db 226 FHGIPTPLVQWVGTFVSVNRID--GILHITTTTLE---PWTNSTIHLIWEPRKIILTLR 280
QY 351 -----SVHYK-----GLISTAFSNGAFGI---GITALLFL-CLALLIKTL--- 389
Db 281 CEGKNQYGVHASFRLPLDPKSSVSVFLRGLQIGIVGAIASALFLFVLVVKMLNMW 340
QY 390 PKRRT-QETPRP 401
Db 341 EENQTCNKKEAPTP 354

RESULT 13
Q13854 PRELIMINARY: PRT: 461 AA.
ID 013854:
AC 013854:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Biliary glycoprotein.
GN BGP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89139550; PubMed=2537311;
RX Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA Eiting J.J., Kamarck M.E.,
RT "Carcinoembryonic antigens: Alternative splicing accounts for the
RT multiple mRNAs that code for novel members of the carcinoembryonic
RT antigen family.";
RL J. Cell Biol. 108:267-276(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA KUROKI M., Matsuo Y., Misumi Y., Oikawa S., Matsuoka Y.;
RT "A new isoform of human biliary glycoprotein (BGP) containing a domain
RT encoded by an Alu-like sequence.";
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: D12502; BAA02063.1;
DR InterPro: IPR001589; Actbind_actnln.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00408; IgC2; 1.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PSS0835; IG_LIKE; 2.

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KW	Immunoglobulin domain
SQ	SEQUENCE 461 AA; 50298 MW; 4A6F0F058B4C727 CRC64;
	Query Match 7.2%; Score 195.5; DB 4; Length 461; Best Local Similarity 21.7%; Pred. No. 1,8e-08; Matches 126; Conservative 77; Mismatches 166; Indels 209; Gaps 30.
OY	5 LLLSSLLGSGAMDCRFKIRVOESVMPEGLICISVP-----CSFSYPRDDMTGSTPAY 57
DB	19 LLTSLIL-----TFNMPPPTTLQDLTESMFPNFAEKGELLVHLNLPQQ-----LF 63
OY	58 GI-VFKAVETTTKAPPAVINHQSFREVENSTGRQLTGDPAKG-----NCSLVTRAQ 109
DB	64 GISYWKG--EAYVDG-----NQIYGAIQTQATGTGPANNSGRETIYPNASLLIQNT 113
OY	110 MODSOFEFRRERGSYYVRNFPMNGDFLTKALTOKRPVYIIPETLEPGQPVYICVFMA 169
DB	114 QNDIGFTLIQV-----IKSDLVNE-----EAIGQFNHY----- 141
OY	170 FEECPSPFSWTGAALLSSQGTRPPTSHTSEVLSFTPRPDHDTLCHVDFSRSKVSQAOT 229
DB	142 -PELPKPS-----ISSNNSPVEDKDVA-AFTCEPETQDITYLMWINNQSPLVSP--- 189
OY	230 VRLVAAPAARPL-VIISIRNDTPPPPEMLRPNVSOANT--VLENLGCTSLPYLE---- 282
DB	190 -RIOLSNCRRLTLLSVLRNDTGYECEIQNPVS-ANBSDPVTLVNTVGGPPTITSPSYT 247
OY	283 ----GOSLCIVCYTHSSPPARLSVNRQGVLSPPSQSPGVLELPVQVEHEGEFTCHAR 338
DB	248 YRRGANLSLSCLYAASNRPADYSMLINLTPOOSTQE-----LFIPIYINNSGSYTCNAN 302
OY	339 HPL-GSOHVSLSLSHVHK-----GLISTAF-----SN 365
DB	303 NSVTGCNRTTYKTIIITERQNLTMLPGDSNSMAQALIPVSQSAREITDNALPQENGSLP 362
OY	366 GAFLG--IGITALLEFLCALIMIL-----PKRTOETEPFRPRSSTIIDYINV 415
DB	363 GAIGIYIGVALVAL-LAAVALAGFLHGKTKGRASDOQDLTE-NKPSVSNHTQ--DHSN- 417
OY	416 VPTAGPLAQKNQKATPNSPRTPLPCAPSPESKNKQKYQLPSFEPKASKTAQAEQE 475
DB	418 -----DPPNKMN----- 424
OY	476 SQELRYATLNFPGVRP-RPEARNPK--GITQADYAEVKQ 512
DB	425 ---EVTVSTLNFEAQOPTOPSASPISLATETIIVSEYKKQ 461
RESULT 14	
ID	060430 PRELIMINARY; PRT; 461 AA.
AC	060430;
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	BGF_HUMAN.
GN	BGP1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
RA	Buckhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stiilwagen S.,
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,
RA	Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA	Liu S., Attix C., Andreise T., Frankel M., Amico-Keller G.,
RA	Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA	Krommiller B., Arellano A., Montomey M., Ow D., Nolan M., Trong S.,
RA	Kobayashi A., Olsen A.S., Carranc A.V.,
RT	"Sequence analysis of a 2.5 kb region in 19q13.2 containing a clustered CEA/PSG gene family.";

Query Match	7.2%	Score 194.5	DB 4	Length 461
Best Local Similarity	21.2%	Pred. No. 2,3e+08		
Matches 123	Conservative 73	Mismatches 175	Indels 209	Gaps 28
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.				
DR EMBL: AC004785; AAC18433.1; -				
DR InterPro: IPR001589; Actbind_actu1n.				
DR InterPro: IPR007110; Ig-like.				
DR InterPro: IPR003598; Ig_c2.				
DR InterPro: IPR003006; Ig_MHC.				
DR Pfam: PF00047; Ig_3.				
DR SMART: SM00408; Igc2_1.				
DR PROSITE: PS00019; ACTININ_1; 1.				
DR PROSITE: PS50835; IG_LIKE; 2.				
DR Immunoglobulin domain.				
KW SEQUENCE 461 AA; 50349 MW; E7810D2559DF7A6F CRC64;				
Query Match	7.2%	Score 194.5	DB 4	Length 461
Best Local Similarity	21.2%	Pred. No. 2,3e+08		
Matches 123	Conservative 73	Mismatches 175	Indels 209	Gaps 28
5 LLLSLGLGSGQAMDGFWIRQVESVMPREGICISYP-----CSFSYPRQDMTGSPYAY 57				
19 LLLTASL-----TFNMPPTTQTLTSPSPFNVAEGEKVLLVHNLPQO-----LF 63				
QY 58 GY-NPKATETTKGAPVATNHQSPREVEMSTGRQLTGDPKAGS-----NCSLYIRDAQ 109				
DB 64 GYSWKG--EKVDG-----NRQVGYAIGTQATPGPNNSGRETITYPASLLIQVNT 113				
QY 110 MODESQYFFRVERGSYVRNPNMNDGFFLKATLTALQKPDVYIPETLEGPQVYICVFNMA 169				
DB 114 QNDGFGYTLQV-----IKSDLVNE-----EATGQFHYV----- 141				
QY 170 FEEDCPSPFSMTGAAALSQGRKPTTSHFSVLSFTPRQDHTDLTCHVDFSRKGVSAORT 229				
DB 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFCEPETQDTYTLMWNNOSLPVSP-- 189				
QY 230 VRLRAVYAPRDL-VISISRDNTPOPENLRLVWVSQANT--VLENIGNGTSLPYE---- 282				
DB 190 -RLQSLNGNRLLTLLSYTRNTGPRECIQNPVS-ANNSDPVTLVNTYGTGPPPTISPSDT 247				
QY 283 ---GQSICLCVYTHSSPPARLSWTORGVLSPSQSDPGVLELPRVOVEHEGEFTCHAR 338				
DB 248 YRRGANLSLSCYAASNPPAQYSWLINGTFQDSQNE-----LFIPIVNNSGSYTCH- 301				
QY 339 HPLGSQHVSLSHYKKGILSTAFSNGAFIGITGALLFLCLALILIKILPKRTQIET 398				
DB 302 -----NNSVTGNCMTYTKT-----ITYERONLTML 327				
QY 399 PR-----PFSRSTILDYINVVPAGPLAQRNOKATPNSPRPLPCA----- 443				
DB 328 PRLDNSMAQALILPSVSQSAEITD--NALPOENGIS-----FOALNGI 368				
QY 444 -----PSPESKKNOKKOYOLPSPPEKSSTO--APESOE 475				
DB 369 VIGVVALVALVALACFLHFGKGTGRASDAQDGLTEHK-----PVSVNHQDHSNDPNN 421				
QY 476 SOEELHYATLNPFGVRP-RPAPAPK--GTQADVAEYVFO 512				
DB 422 KMEVYTYSTLNFEAQPTQPTSPASPSLATATEIIFYSEVKK 461				
RESULT 15				
Q8R007				
ID Q8R007	PRELIMINARY;	PRF:	508 AA.	
AC Q8R007;				
DT 01-JUN-2002 (TREMBLrel. 21, Created)				
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE Similar to poliovirus receptor-related 4 (Necclin 4).				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_Taxid=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA Strausberg R.;				

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 20:01:08 : Search time 23 Seconds

(without alignments)
941.876 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGSGQAMDR.....RPEARMPKGTQADYAEVKRQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	888	32.8	431	3	US-09-038-832-2
2	888	32.8	431	3	US-09-038-832-4
3	831.5	30.7	467	3	US-09-046-736-2
4	769	28.4	440	3	US-08-759-628-4
5	693.5	25.6	421	3	US-08-759-628-5
6	573	21.2	374	3	US-09-046-736-4
7	177.5	6.6	501	2	US-08-408-095-31
8	172.5	6.4	403	4	US-09-638-649-5
9	167	6.2	464	2	US-08-602-725-32
10	155	5.7	321	6	5168835-17
11	153.5	5.7	416	4	US-09-638-649-1
12	152.5	5.6	373	4	US-09-996-243-503
13	151.5	5.6	1241	3	US-09-040-774-2
14	143	5.3	642	1	US-08-217-299-1
15	143	5.3	698	2	US-08-602-725-36
16	143	5.3	734	2	US-08-389-459A-17
17	143	5.3	734	2	US-08-987-867A-17
18	139.5	5.2	611	2	US-08-752-307B-10
19	139.5	5.2	611	4	US-09-707-802-10
20	139.5	5.2	611	4	US-09-991-326-10
21	139	5.1	404	4	US-09-638-649-3
22	138	5.1	354	6	5168835-4
23	136.5	5.0	432	4	US-09-778-510-2
24	136	5.0	1091	3	US-08-986-485-5
25	135.5	5.0	630	2	US-08-752-307B-14
26	135.5	5.0	630	4	US-09-707-802-14
27	135.5	5.0	630	4	US-09-991-326-14

28	134.5	5.0	398	4	US-09-778-510-6	Sequence 6, Appl
29	132.5	4.9	972	3	US-08-750-141A-2	Sequence 2, Appl
30	132	4.9	647	5	PCT-US93-00031-23	Sequence 2, Appl
31	132	4.9	828	1	US-08-261-304-2	Sequence 2, Appl
32	131.5	4.9	1260	4	US-08-506-296B-21	Sequence 21, Appl
33	130.5	4.8	946	5	PCT-US95-08493-13	Sequence 13, Appl
34	130	4.8	408	4	US-09-724-864-62	Sequence 62, Appl
35	129	4.8	612	2	US-08-359-705B-8	Sequence 8, Appl
36	129	4.8	612	2	US-08-286-846A-8	Sequence 8, Appl
37	129	4.8	612	2	US-08-457-880A-8	Sequence 8, Appl
38	129	4.8	612	3	US-08-444-622A-8	Sequence 8, Appl
39	129	4.8	612	3	US-08-942-562-8	Sequence 8, Appl
40	129	4.8	612	3	US-09-156-923-8	Sequence 8, Appl
41	129	4.8	739	4	US-08-482-073-6	Sequence 6, Appl
42	129	4.8	739	5	PCT-US93-00031-9	Sequence 9, Appl
43	129	4.8	839	2	US-08-359-705B-6	Sequence 6, Appl
44	129	4.8	839	2	US-08-286-846A-6	Sequence 6, Appl
45	129	4.8	839	2	US-08-457-880A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-038-832-2

Sequence 2, Application US/09038832

Patent No. 6146845

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

APPLICANT: ERICKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-2

TITLE OF INVENTION: (SAF-2)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA

STREET: P.O. Box 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTED for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038, 832

FILING DATE: 11-MAR-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/041, 886

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ. ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-038-832-2

Query Match 32.8%; Score 888; DB 3; Length 431;
Best Local Similarity 47.8%; Pred. No. 9.8e-70;
Matches 195; Conservative 52; Mismatches 127; Indels 34; Gaps 6;


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX05520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-759-628-5

Query Match      25.6% Score 693.5; DB 3; Length 421;
Best Local Similarity 43.0%; Pred. No. 11e-52;
Matches 157; Conservative 53; Mismatches 132; Indels 23; Gaps 4;

QY 3 LPILLSLL-GGSQAMDRFWIRVOESYVWVEGLCISVPCFSFSPRODWTGSTPAYGYWF 61
DB 1 MLLLLPLMLGSSLDKRPVYELQVKSVYQEGLCVLPCSFSTYWRMYSSPPLYTWFF 60
QY 62 KAVTTTGAPVATNHOSEYEMSTRGRFOLTGPDAKNCSLVTRDAOMODESOYFFRVE 121
DB 61 RDGEIPYAEVVAATNPNRVRKPEYQGRFLGDVQKKNCSLSIGDAMHEDTGSYFFRVE 120
QY 122 RGSYRVNFMNDGFLLKVTALTKQPDVYIPELTPG--QPVTVICVFMMAFEECPSPFS 179
DB 121 RGRDVKYSQGNKMLNLETALIEKPDHLSGPLSGMLKPTRLSCSLPGSCVAGPILTF 180
QY 180 WTGAALSSQGTKPTTSHFSVLSFTPRPDHDTLTCVHDFSRKGSQAORTVRLKAAVAPR 239
DB 181 WTGNAXSAPWT-PRXAPRELTLTPRPEDHGTNLTCQKRGQAQVTTETXVOLVNSAPQ 239
QY 240 DLVLSISNDNTPDPPELNRVMSQANRTVLENLNGTSLPVLEQSLCLVCTHSSPPAR 299
DB 240 TITTF-----RNGIALETILQNTSYLPLEGQALRLICDADSPFAH 280
QY 300 LSWTORGVLSPSQSDPGVLELPRVOYEHGEFTCHARHPLGSOHSLSTVYKKGGLI 359
DB 281 LSWRQGSAPALNATISNTGILKRVKSAEBGFTCRARQHPGLQIFNLISVSLPOL 340
QY 360 STAFS 364
DB 341 GPSCS 345

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```

APPLICANT: KIKLY KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-046-736-4

Query Match      21.2% Score 573; DB 3; Length 374;
Best Local Similarity 29.8%; Pred. No. 3.6e-42;
Matches 156; Conservative 63; Mismatches 138; Indels 166; Gaps 10;

QY 2 LPLILLSLGGQAMGR-----FWIRVOESYVWVEGLCISVPCFSFSPRODWTGSTP 55
DB 1 MLLLLPLMLGRERVRQKSNRKYDSTLWQSVYQEGMCVHRCFSFSPVDQSDSDP 60
QY 56 AYGWAFKAVTETTGKAVATNHOSEYEMSTRGRFOLTGPDAKNCSLVTRDAOMODESQ 115
DB 61 VHGWFRAQNDISKAKAVATNPNRVAIVQETRDFHLSDPQTKNCTLSIRDAKMSDAGR 120
QY 116 YFRFVEGSAVRKFMNDGFLLKVTALTKQPDVYIPELTPGQPVTVICVFMMAFEECP 175
DB 121 YFRFMEKGN-IKWNYKKDQLSVNVTY----- 145
QY 176 PFSWGTGAALSSQGTKPTTSHFSVLSFTPRPDHDTLTCVHDFSRKGSQAORTVRLRVA 235
DB 146 ----- 145
QY 236 YAPRDVLSISRNDTPDPPELNRVMSQANRTVLENLNGTSLPVLEQSLCLVCTHSS 295
DB 146 -----PQGNLVTVTFQSGSTALNGSSSLVLEGGSLRLVCAYDSN 188
QY 296 PPARLSWTORGVLSPSQSDPGVLELPRVOYEHGEFTCHARHPLGSOHSLSTVYK 355
DB 189 PPARLSWTWRSLLTSPSQSNPLVLEL-QVHLDEGEFTCRARQNSLSGSHVSLNLSLOE 247
QY 356 -----KGLISTARNSGAFIGITALLFLCLALIMKILPKRRTQETPRPRSRKS 407
DB 248 YTKKMPVSGVLL-----GAVGAGATLAFVLSFCVIFIV--RSCRKKSAP----- 293
QY 408 TILDYINVTAGPLAQKRNOKATPNSPRTPLPGAPSPESKKNOKQQLVPSFPKSS 467

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RESULT 6
US-09-046-736-4
Sequence 4, Application US/09046736
Patent No. 6090582
GENERAL INFORMATION:

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Db 294 -----ADVDIDMK-----DANTINGSASOGUFTSMADDPNRH 329
QY 468 TQAPESQSEELHYATLNPFGVRRPEARMKGTQADYAEVK 510
Db 330 GLAAHSSGERETQVAPLSPHKGEPQ-DLSGQATNNEXSEIK 371

RESULT 7

US-08-408-095-31
; Sequence 31, Application US/08408095
; Patent No. 585678
; GENERAL INFORMATION:
; APPLICANT: Chinadural, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MTON, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,095
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-408-095-31

Query Match 6.6%; Score 177.5; DB 2; Length 501;
Best Local Similarity 20.0%; Pred. No. 2,8e-07;
Matches 107; Conservative 82; Mismatches 182; Indels 165; Gaps 24;

QY 25 VQESVAVPGLCTSVPCSF-----SYPRDDMTGSTRAYGYWFAVETTTGAVVANNHOS 79
Db 80 IQMPPIREGDVTLCNTNNSNPSVTRTEM---KPGAMEEPLSGVLTQVQWDMNTT 135
QY 80 REVENSTRGRFOLTGPARGNCSLVIRDAQOMODESOYFFRVERGSYVYRNFMDGFLKY 139
Db 136 --TACARCNSMCSMASPVALNVQYAPRDVRR-----KI 167
QY 140 TALTORPDYIPTLEPGQPVYIYCFNNAFECCPPPSRW---TGAALSSQGTPTTSHF 197
Db 168 KPLSE-----IHSGNSVSLQCDPSSHPK--EVOEFMEKNRGLG---KESQOLNF 212
QY 198 SVLSFTPRPDHDTDLTCHVDPSRKGVSAQRTVRLVAAYAPRDVVISISRDNPDPDENL 257
Db 213 DSI-----PEDAGS-YSCHVNNNS-IGQTASKANTLLEVLAAPRLRVSMSFGD----- 258
QY 258 RVNVAQANRTVLNENLNGTSLPYLEGOISLCLVCTHSSPPAR-----LSWTORQOVLSPSQ 313
Db 259 -----QVMEGKSATLTCESDANPVPVSHYTWFDMMNQ-----SL 291
QY 314 PSDPGVLELPRVOVEHEGEFTCHARRPLGSOHVSLS-LSVHYKKGLISTAFSGAFLGIG 372
Db 292 PHSORLRLPEVAVOHSGAVWCQGTNSVGGRSPLSLTLYVYSPETI-----GRVAVG 345

QY 373 ITALLFLCALIIMKI-----LPKR--RTQET-----PRPRFSRHSHIILYIN 414
Db 346 LGS-----CLATILALICGLKLORRMKTQSOGLQENSQSFVFNKKVRRAPLISGPH 401
QY 415 VDPAGPLAQKRNQKATPNPSPRPLPGAPSPSK-----KNOKROY 456
Db 402 SLGCYNPMWMDGISYTLTRPEEMNIPRTGDAESSEMGRRPRTQDDVTYSALKROYGDY 461
QY 457 Q--LPSPPEPKSTQAPESQSEELHYATLNPFGVRRPEARMKGTQADYAEVK 510
Db 462 ENVIPDFPE-----DEGIHYSLEIOFGVERPOAQ-----ENVDYILK 500

RESULT 8

US-09-638-649-5
; Sequence 5, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5

Query Match 6.4%; Score 172.5; DB 4; Length 403;
Best Local Similarity 23.3%; Pred. No. 5,7e-07;
Matches 101; Conservative 46; Mismatches 139; Indels 147; Gaps 21;

QY 100 NCSLVIRDAQOMODESOYFFRV--ERGSYVRNFMNDGFLKYATLQKPDVYIPET-LEP 156
Db 80 NCSLLPLPATGIVEGCFRCRATNRKGEKSNVR---VRVQIPKPEIIVPASLTA 134
QY 157 GQPVTV-ICVFNNAFECCPPPSRW---TGAALSSQGT-----PTSHSPVLS-F 202
Db 135 SVPNKVGTCVSEGSY--PAGTSLMHLGKLLIPDGKETLVKEETRRHHPETGLFTLSEL 191
QY 203 TPAP-ODHDTDLTCHVDPSRKGVSAQRTVRLVAAYAPRDVVISISRDNPDPDENLRVMV 261
Db 192 TVIPTRQGGTTHPFFSGSFS-LGLPRRRPLNT-----APQL-----KVRREGPEGLOLV 241
QY 262 SQANRTVLNENLNGTSLPYLEGOISLCLVCTHSSPPARLSWTORGQVLSPOSPDPGVLE 321
Db 242 EPEGGI-----VAPGGTVTLTCAISAQPPQVHMIRKDAVL-PLAASP--VLL 286
QY 322 LPRVOVEHEGEFTCHARRPLGSOHVSLSVH-----KGLISTAPNSGA 367
Db 287 LPEVGHADBSTYSCVATHPSHGPOESPVSIRVTEGDEGPAAGSVGESGLTALALGI 346
QY 347 LGSLGVALL-----VAILMKR 365
Db 428 QKATPNSPTPLPGAPSPESKNQKQOLPSPPEPKSTQAPESQSEELHYATLNF 487
QY 366 Q-----PREREK-----APEQSEDEE--RAELN- 388
Db 488 PGVRRPEARMK 500
Db 389 -----QSEEAEMPE 397

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RESULT 9
US-08-602-725-32
; Sequence 32, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DUBBIN, HEIGA
; APPLICANT: SNARY, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-602-725-32

Query Match      6.2%; Score 167; DB 2; Length 464;
Best Local Similarity 23.5%; Pred. No. 2.1e-06;
Matches 85; Conservative 52; Mismatches 122; Indels 102; Gaps 18;

QY 5 LLSLSLGGSGAQMGRFIRQESVMPEGLICIVP-----CSFSYPRQDWTGSTRPAY 57
   |||||
Db 19 LTRSLSL-----TWNPTTAQLTTESMPFVAGKEVLLVHMLPQQ-----LF 63
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QY 58 GY-WFKAVETTTKGPAPVATNHSREVMSTRGRFOLGDPAGK-----NCSLYTRDAQ 109
   |||||
Db 64 GYSWYKG--ERYVDG-----NRQIVGAYLIGQOATPGPANGSRETIYFNASLLIONVT 113
   |||||

QY 110 MDESQYFFRYKRSYRYNFMNDGFLLKVTALTOKPDVYIPETLEPGQPVTVICVFNMA 169
   |||||
Db 114 QNDTGFYTLQY-----IKSDLVNE-----EATGQFHYV-----141
   |||||

QY 170 FECCPPPSFSMTGAALSSQGTKPTTSHFSVLSFTPRQDDTDLTCHVDSRKGYSAQRT 229
   |||||
Db 142 -PELPKRS-----ISSNNSNVEDKDAY-AFTCEPEYDVTYLMWINNQS.LPVPSP--- 189
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QY 230 VRLRVAYAPRDL-VISISRDNTPDPENLKVAVSQANRT--VLENLGNSTSLPYLE----- 282
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Db 190 -RLQLSNGNRTLLTSLVTRNDTGPYCEIQNPNVS-ANRSDPYTLNWTGPDPTTISPST 247
QY 283 ----GQSICLVCTHSSPPARLSWTQRCQVLSPPSDPGVLELPRVOHEHGEFTCHAR 338
   |||||
Db 248 YRRPGANLSTSCYAASNPPAQYSWMLNGTFQOSTOE-----LFIPIITVNNSGSYTCHAN 302
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QY 339 H 339
Db 303 N 303

RESULT 10
5169835-17
; Patent No. 5169835
; APPLICANT: MAI-YEE, CHAN
; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEIN APPLICATIONS
; NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/390,409
; FILING DATE: 07-AUG-1989
; SEQ ID NO:17:
; LENGTH: 321
5169835-17

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Query Match      5.7%; Score 155; DB 6; Length 321;
Best Local Similarity 24.3%; Pred. No. 1.4e-05;
Matches 73; Conservative 43; Mismatches 105; Indels 80; Gaps 15;

QY 58 GY-WFKAVETTTKGPAPVATNHSREVMSTRGRFOLGDPAGK-----NCSLYTRDAQ 109
   |||||
Db 64 GYSWYKG--ERYVDGNSLIVG-----VIGQOATPGPANGSRETIYFNASLLIONVT 113
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QY 110 MDESQYFFRYKRSYRYNFMNDGFLLKVTALTOKPDVYIPETLEPGQPVTVICVFNMA 169
   |||||
Db 114 QNDTGFYTLQY-----IKSDLVNE-----EATGQFHYV-----141
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QY 170 FECCPPPSFSMTGAALSSQGTKPTTSHFSVLSFTPRQDDTDLTCHVDSRKGYSAQRT 229
   |||||
Db 142 -PELPKRS-----ISSNNSNVEDKDAY-AFTCEPEYDVTYLMWINNQS.LPVPSP--- 189
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QY 230 VRLRVAYAPRDL-VISISRDNTPDPENLKVAVSQANRT--VLENLGNSTSLPYLE----- 282
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Db 190 -RLQLSNGNRTLLTSLVTRNDTGPYCEIQNPNVS-ANRSDPYTLNWTGPDPTTISPST 247
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QY 283 ----GQSICLVCTHSSPPARLSWTQRCQVLSPPSDPGVLELPRVOHEHGEFTCHAR 338
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Db 248 YRRPGANLSTSCYAASNPPAQYSWMLNGTFQOSTOE-----LFIPIITVNNSGSYTCHAN 302
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QY 339 H 339
Db 303 N 303

RESULT 11
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 05/5/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 416
; TYPE: prt
; ORGANISM: Bos Taurus

```


TITLE OF INVENTION: Nephrlin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, Suite 3200
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 97,842
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-040-774-2

Query Match 5.6%; Score 151.5; DB 3; Length 1241;
Best Local Similarity 22.2%; Pred. No. 0.0002;

Matches 89; Conservative 55; Mismatches 146; Indels 111; Gaps 17;

QY 1 MLPLLLSLV--LGSQAMDGKRFVIRVQESVWVPEGICISVPCSFYPRQDWTGSPAYG 58
DB 12 LLLGLTLEGLAQALTAIVASVPRGW-ALPENTLVVEGASVLRGCVSTP-----GSAV--- 62
QY 59 YWEK-----AVYETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMODE 113
DB 63 QMAKDGILLGPDRIPIGFP-----RYRLGDPARGFHLHICADLSD 106
QY 114 SQFFVERGSGYRIVFMNDGFLLKYTA-----LTQRPDYIIPTELEPGQVYVICYPMNA 169
DB 107 AEVCCQYR-SEMGPELVSPRYLLSLVPPKLLLTPEAGTWTWVAGQEVVNCVSGDA 165
QY 170 FECCPPPSFWSGTGAALSOGTKPTTSHFVLSFTPRQDHDITLCHVD--FSKGVSAQ 227
DB 166 -KAPDITILLSCQITIS-----DISANVNGSQQKLEIYE 199
QY 228 RTVRLVAYAPRDVLVISRDNTPDPPELRLVWVSOANRTVLE-----NIGNGTSL 278
DB 200 ATARV-----TPRSSDNQQLLVCEASSPALEAPTKASPTVAVLPPGP 242
QY 279 PVLE-----GQSILCVYTH--SSPPARLSMTQKQVSP-----SOPSDPGVL 320
DB 243 PVLEWPGLEGHVRAOQSLTEPCVARGGNPLATLQWIKNGQPVSTAMGTEHTQAVARSYL 302
QY 321 ELPRVOVEHEGFEFTCHARHPL--GSOHVSLSLVHYKKGLI 359
DB 303 VMTVREDHCAQLSCAHSNVSAGTQEHGTLTLOYTTPPSAI 343

RESULT 14
US-08-217-299-1
Sequence 1, Application US/08217299
Patent No. 5672513
GENERAL INFORMATION:
APPLICANT: Mach, J. P.
APPLICANT: Pelegriin, A.

APPLICANT: Tersklkh, A.
TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93810214.2
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 4093/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-3500
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-217-299-1

Query Match 5.3%; Score 143; DB 1; Length 642;
Best Local Similarity 21.3%; Pred. No. 0.00043;

Matches 87; Conservative 53; Mismatches 143; Indels 126; Gaps 18;

QY 57 YGY-WFKAVYETTKGAPVATNHQSRVEMSTRGRFQLTGDPAGK-----NCSLVIRDA 108
DB 29 FGYSWYKG--ERVDG-----NRQIGVYIGTQATTPGPAVSGRRIIYPMNSLIGNI 78
QY 109 QMODESOYFRVERGSGYRIVFMNDGFLLKYTA--LTQRPDYIIPTELEPGQVYVICYPMNA 168
DB 79 IQNDTGFYTLHVTKSDLV--NEEATGQFR----- 105
QY 169 AFEECPSPFSWGTGAALSOGTKPTTSHFVLSFTPRQDHDITLCHVDFSKGVSAQR 228
DB 106 VPELEKPPS-----ISSNNSKPVEDKDAV-AFTCEPEQDATTYLMVWVNSQLPVSF 155
QY 229 TVRLVAYAPRDVLVI--SISRDNTPD--PPENLRYVWVSOANRTVLENLNGTSLPVL----- 281
DB 156 --RLQLSNGMRITLTLFVNTVNDTASYKCEIQYNVARSRSVLTAVLYGDPATLISPLNT 213
QY 282 ---EGOSLCLVCYTHSSPPARLSMTQKQVLSQSPSDPGVLELPRVOVEHEGFEFTCHAR 338
DB 214 SYRSGENLNLSCAASNPAPQYSFVNGTFQOSTOE---LFIPNTVNNSSGYTCQAH 268
QY 339 HPLGSOHVSLSLVHYKKGLISTAFNSGAPLIGITALLPLCLALLIMKILPRRRQOTET 398
DB 269 NS-----DTGLNRTT-----VTIT-----TYAEP 288
QY 399 PRPRFSRHSF--ILDYINNVPTAGPLAOKR-----NOKATPNSPRTPL 439
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 20:02:07 : Search time 46 Seconds
(without alignments)
1793.429 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGSGQAMDGR.....RPEARMPKGTQADVAEVKRP 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by the result to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2580.5	95.4	697	11 US-09-910-600-28	Sequence 28, App1
2	2576.5	95.2	697	11 US-09-984-130-149	Sequence 149, App
3	2278	83.7	544	11 US-09-910-600-8	Sequence 8, App11
4	2265	83.7	544	10 US-09-978-295A-259	Sequence 259, App
5	2265	83.7	544	10 US-09-978-697-259	Sequence 259, App
6	2265	83.7	544	10 US-09-978-192A-259	Sequence 259, App
7	2265	83.7	544	10 US-09-999-832A-259	Sequence 259, App
8	2265	83.7	544	11 US-09-978-189-259	Sequence 259, App
9	2265	83.7	544	11 US-09-978-608A-259	Sequence 259, App
10	2265	83.7	544	11 US-09-978-585A-259	Sequence 259, App
11	2265	83.7	544	11 US-09-978-191A-259	Sequence 259, App
12	2265	83.7	544	11 US-09-978-403A-259	Sequence 259, App
13	2265	83.7	544	11 US-09-978-564A-259	Sequence 259, App
14	2265	83.7	544	11 US-09-999-833A-259	Sequence 259, App
15	2265	83.7	544	11 US-09-981-915A-259	Sequence 259, App

16	2265	83.7	544	11 US-09-978-824-259	Sequence 259, App
17	2265	83.7	544	11 US-09-918-585A-259	Sequence 259, App
18	2265	83.7	544	11 US-09-978-423A-259	Sequence 259, App
19	2265	83.7	544	11 US-09-978-193A-259	Sequence 259, App
20	2265	83.7	544	11 US-09-999-830A-259	Sequence 259, App
21	2265	83.7	544	11 US-09-978-837A-259	Sequence 259, App
22	2265	83.7	544	11 US-09-978-187B-259	Sequence 259, App
23	2265	83.7	544	11 US-09-978-643A-259	Sequence 259, App
24	2265	83.7	544	12 US-09-978-375A-259	Sequence 259, App
25	2265	83.7	544	12 US-09-978-188A-259	Sequence 259, App
26	2265	83.7	544	12 US-09-978-296A-259	Sequence 259, App
27	2265	83.7	544	12 US-10-143-031A-259	Sequence 259, App
28	2265	83.7	544	12 US-10-002-967A-259	Sequence 259, App
29	2265	83.7	544	12 US-10-017-083A-259	Sequence 259, App
30	2265	83.7	544	12 US-10-143-030A-259	Sequence 259, App
31	2265	83.7	544	12 US-10-199-672-118	Sequence 118, App
32	2265	83.7	544	12 US-10-187-749-118	Sequence 118, App
33	2265	83.7	544	12 US-10-194-457-118	Sequence 118, App
34	2265	83.7	544	12 US-10-145-128A-259	Sequence 259, App
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36	2265	83.7	544	12 US-10-196-747-118	Sequence 118, App
37	2265	83.7	544	12 US-10-173-688-118	Sequence 118, App
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39	2265	83.7	544	12 US-10-173-691-118	Sequence 118, App
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41	2265	83.7	544	12 US-10-173-694-118	Sequence 118, App
42	2265	83.7	544	12 US-10-173-698-118	Sequence 118, App
43	2265	83.7	544	12 US-10-173-699-118	Sequence 118, App
44	2265	83.7	544	12 US-10-173-707-118	Sequence 118, App
45	2265	83.7	544	12 US-10-174-569-118	Sequence 118, App

ALIGNMENTS

US-09-910-600-28	RESULT 1
Sequence 28, Application US/09910600	
PUBLICATON NO. US20030036631A1	
GENERAL INFORMATION:	
APPLICANT: Longphre, Mallinda	
APPLICANT: Chang, Han	
APPLICANT: Whitney, Gena	
TITLE OF INVENTION: NOVEL SIEGLES AND USES THEREOF	
FILE REFERENCE: D0003NP	
CURRENT APPLICATION NUMBER: US/09/910.600	
CURRENT FILING DATE: 2001-07-20	
PRIOR APPLICATION NUMBER: 60/220.139	
PRIOR FILING DATE: 2000-07-21	
NUMBER OF SEQ ID NOS: 32	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 28	
LENGTH: 697	
TYPE: PRT	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Description of Artificial Sequence: L3-995-2	
US-09-910-600-28	
Query Match	95.4% Score 2580.5; DB 11; Length 697;
Best Local Similarity	73.2% Pred. No. 3.9e-195;
Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;	
QY	1 MLPLLLSLGSGQAMDGRFWIRVDSVWVPGCLISVPCSFYPRDWTGSTPAYGV 60
DB	1 MLPLLLSLGSGQAMDGRFWIRVDSVWVPGCLISVPCSFYPRDWTGSTPAYGV 60
QY	61 FKAVETTGAPATNHSREVMSTRGRFOLGDAKGCSTVIRDAQMDSSQYFFRV 120
DB	61 FKAVETTGAPATNHSREVMSTRGRFOLGDAKGCSTVIRDAQMDSSQYFFRV 120
QY	121 ERGSYRVNFMNDGFELKVTALPQKPDVYIPETLEFGQPVTVYCVENMAFECPSPFSFM 180

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Db 121 ERGSYVRNENMGDFFLKVTALITQKPDVYIPETLEPGQPVYICVFNMAFECECPPSFSW 180
QY 181 TGAALSSOGTKPTTSHFSVLSFTPRPODHDLDLCHVDFSRKGSAGRTVRLRAYAPRD 240
Db 181 TGAALSSOGTKPTTSHFSVLSFTPRPODHDLDLCHVDFSRKGSAGRTVRLRAYAPRD 240
QY 241 LVISISDNTPD----- 252
Db 241 LVISISDNTPD----- 252
QY 253 -----PENLRVWVSOANRTYLE 270
Db 301 WGRPRGLLELPGVKAQDSGRYTCRAENRLGSGQRALDLSVQPPENLRVWVSOANRTYLE 360
QY 271 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSQSPGVLELPRVQVEHE 330
Db 361 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSQSPGVLELPRVQVEHE 420
QY 331 GEFTCHAHRLPGSOHVSLSLVHY----- 354
Db 421 GEFTCHAHRLPGSOHVSLSLVHYSPKLLGPSCSWEAEGLHCSSQASAPSLRWMLGE 480
QY 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGPMANSSLSHGGLSSGLRLCEAMNVHGAQSGSIILQLPDK 540
QY 356 KGLISTAFSNGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYINV 415
Db 541 KGLISTAFSNGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYINV 600
QY 416 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEPKSSTQAPESQ 475
Db 601 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEPKSSTQAPESQ 660
QY 476 SOEELHYATLNFPGVRRPREARMKGTQADYAIVKFO 512
Db 661 SOEELHYATLNFPGVRRPREARMKGTQADYAIVKFO 697

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102(e)

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RESULT 2
US-09-984-130-149
; Sequence 149, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-149

```

Query Match 95.2%; Score 2576.5; DB 11; Length 697;
Best Local Similarity 73.0%; Pred. No. 8,2e-195;

Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

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QY 1 MLPLILSLGSGQAMDGFRFWLRVDSVWVPEGLICISVPCSFSTYPRQDWTGSTPAYGYW 60
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Db 1 MLPLILSLGSGQAMDGFRFWLRVDSVWVPEGLICISVPCSFSTYPRQDWTGSTPAYGYW 60
QY 61 FFAVETTKGAVATNHQSRVEMSTRGFFOLTGPANGNSLVTRDQMDQESQYFPRV 120
Db 61 FFAVETTKGAVATNHQSRVEMSTRGFFOLTGPANGNSLVTRDQMDQESQYFPRV 120
QY 121 ERGSYVRNENMGDFFLKVTALITQKPDVYIPETLEPGQPVYICVFNMAFECECPPSFSW 180
Db 121 ERGSYVRNENMGDFFLKVTALITQKPDVYIPETLEPGQPVYICVFNMAFECECPPSFSW 180
QY 181 TGAALSSOGTKPTTSHFSVLSFTPRPODHDLDLCHVDFSRKGSAGRTVRLRAYAPRD 240
Db 181 TGAALSSOGTKPTTSHFSVLSFTPRPODHDLDLCHVDFSRKGSAGRTVRLRAYAPRD 240
QY 241 LVISISDNTPD----- 252
Db 241 LVISISDNTPD----- 252
QY 253 -----PENLRVWVSOANRTYLE 270
Db 301 WGRPRGLLELPGVKAQDSGRYTCRAENRLGSGQRALDLSVQPPENLRVWVSOANRTYLE 360
QY 271 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSQSPGVLELPRVQVEHE 330
Db 361 NLGNSTSLPVLGEGSLCLVCTHSSPPARLSWTORGQVLSPPSQSPGVLELPRVQVEHE 420
QY 331 GEFTCHAHRLPGSOHVSLSLVHY----- 354
Db 421 GEFTCHAHRLPGSOHVSLSLVHYSPKLLGPSCSWEAEGLHCSSQASAPSLRWMLGE 480
QY 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGPMANSSLSHGGLSSGLRLCEAMNVHGAQSGSIILQLPDK 540
QY 356 KGLISTAFSNGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYINV 415
Db 541 KGLISTAFSNGAFIGITALLFLCLALLIMKILPKRRTQETPRPRFSRSHSTIIDYINV 600
QY 416 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEPKSSTQAPESQ 475
Db 601 VPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKKNOKQOYLPSFPEPKSSTQAPESQ 660
QY 476 SOEELHYATLNFPGVRRPREARMKGTQADYAIVKFO 512
Db 661 SOEELHYATLNFPGVRRPREARMKGTQADYAIVKFO 697

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RESULT 3
US-09-910-600-8
; Sequence 8, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gene
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-600-8

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Query Match 84.2%; Score 2278; DB 11; Length 544;
Best Local Similarity 75.1%; Pred. No. 2.1e-171;

Matches 452; Conservative 1; Mismatches 1; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSGQAMDRFWIRVOESVYVPEGLCISVPCSESYPRODWTGSTPAYGW 60
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QY 61 FKAVTETTKAPVATNHOSEVEMSTRGRFOLTGDPAKNCSLVIRDAQMODSSQYFRV 120
DB 61 FKAVTETTKAPVATNHOSEVEMSTRGRFOLTGDPAKNCSLVIRDAQMODSSQYFRV 120
QY 121 ERGSYRYNFMNGFELKATNALOKPDVYIPETLEBQPTVYLCVFMAEECPPEPSFW 180
DB 121 ERGSYRYNFMNGFELKATNALOKPDVYIPETLEBQPTVYLCVFMAEECPPEPSFW 180
QY 181 TGAALSSQGTKPTTSHFSVLEFMPRODHTDLTCHVDFSRKGSQAORTVRLVAYAPRD 240
DB 141 -----VLSFTPRPDHNTDLCHVDFSRKGSQAORTVRLVAYAPRD 182
QY 241 LVISIRSDNTPD----- 252
DB 183 LVISIRSDNTPALEPOQGNVPLYEAQKQOFLRLCAADSQPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVAVSQANRTVLE 270
DB 243 WGPRLGLELPGVKADDSGRYTCRAENRLGSGQARALDSVQYPPENLRVAVSQANRTVLE 302
QY 271 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSMTORGCVLSPSPDPGVLELPRVOYEHE 330
DB 303 NLGNGTSLPYLEGOSLCLVCTHSSPPARLSMTORGCVLSPSPDPGVLELPRVOYEHE 362
QY 331 GEFTCHARRHPLGSGQHWLSLSVHYKKGLISTAFSNGAFIGITALLFLCLALIMKILP 390
DB 363 GEFTCHARRHPLGSGQHWLSLSVHYKKGLISTAFSNGAFIGITALLFLCLALIMKILP 422
QY 391 KRRTOTETPPRRFSRSTIDYINNVPTAGPLAQNRQKTRPSRPLRPGAPSPESK 450
DB 423 KRRTOTETPPRRFSRSTIDYINNVPTAGPLAQNRQKTRPSRPLRPGAPSPESK 482
QY 451 NOKKOYQLPSFPKPSSTQAPESQESQELHYATLNEPGVRRPEARMKGTADYAEVK 510
DB 483 NOKKOYQLPSFPKPSSTQAPESQESQELHYATLNEPGVRRPEARMKGTADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 4
US-09-978-295A-259
Sequence 259, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

1 MLPLLLSLILGSGAMGRFWRIRQESVWMPPEGICISVPCSFYPRDDMGSPAGCYW 60
1 MLPLLLSLILGSGAMGRFWRIRQESVWMPPEGICISVPCSFYPRDDMGSPAGCYW 60
61 FKAVETTKGAPVATNHOSEVENSTGRFOLTDGPAKNGSLVIIRDAOMODESOYFRV 120
61 FKAVETTKGAPVATNHOSEVENSTGRFOLTDGPAKNGSLVIIRDAOMODESOYFRV 120
121 ERGSYVRKNEMNDGFEFLKVTALTKPDVYIETLEPGQPVYICVFNNAFEECCPPSSW 180
121 ERGSYVRKNEMNDGFEFLKVTALTKPDVYIETLEPGQPVYIICVFNNAFEECCPPSSW 140
121 ERGSYVRKNEMNDGFEFLKVTALTKPDVYIETLEPGQPVYIICVFNNAFEECCPPSSW 140
181 TGAALSSQGTAKPTSHFSVLSFTPRPODHTDLCVHDSKKGVSQORTVRLRAYAPRD 240
141 -----VLSFTPRPODHTDLCVHDSKKGVSQORTVRLRAYAPRD 182
241 LVISISRDNTPD-----PENLRVWVSQANRYVLE 252
183 LVISISRDNTPDLEPQGNVPLYEAKGQFLRLCAADSOBPATLSVWLNRYLSSSH 242
253 -----PENLRVWVSQANRYVLE 270
243 WGPRLGLELPGVAKGDSGRYTCRAENLGSQORALDISVOY PENLRVWVSQANRYVLE 302
271 NLGNGTSLPYLEGOSLVCVTHSSPPARLSMTORGQVLSOPSOPGVLELPRQVBE 330
303 NLGNGTSLPYLEGOSLVCVTHSSPPARLSMTORGQVLSOPSOPGVLELPRQVBE 362
331 GEFTCHARHPLGSOHVSLSISVHYKKGLISTAFSNGAFUGITALLFLCLALIMKILP 390
363 GEFTCHARHPLGSOHVSLSISVHYKKGLISTAFSNGAFUGITALLFLCLALIMKILP 422
391 KRRTQETPRPRFSGHSTILDIYINVPAGPLAQRNOKATPNSRPTLPBGAPSPESKK 450
423 KRRTQETPRPRFSGHSTILDIYINVPAGPLAQRNOKATPNSRPTLPBGAPSPESKK 482
451 NOKKOYOLPSPPEKSSTOAPESQESQELHYATLNFPGVPRPREARMKGTQADYAEVK 510
483 NOKKOYOLPSPPEKSSTOAPESQESQELHYATLNFPGVPRPREARMKGTQADYAEVK 542

OY 511 FO 512
11
Db 543 FO 544

RESULT 5
US-09-978-697-259
: Sequence 259, Application US/09978697
: Patent No. US20020169284A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumes, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC27
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: 09/918585
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/064249
: PRIOR FILING DATE: 1997-11-03
: PRIOR APPLICATION NUMBER: 60/065311
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: PRIOR APPLICATION NUMBER: 60/079294

: PRIOR FILING DATE: 1998-03-25
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: PRIOR FILING DATE: 1998-04-01
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: PRIOR FILING DATE: 1998-04-08
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: PRIOR APPLICATION NUMBER: 60/081071
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: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085573
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085704
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085697
: PRIOR APPLICATION NUMBER: 60/085697

Query Match      83.7%  Score 2265;  DB 10;  Length 544;
Best Local Similarity 74.8%  Pred. No. 2,36-170;
Matches 450;  Conservative 1;  Mismatches 3;  Indels 148;  Gaps 2;

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RESULT 6
US-09-978-192A-259
: Sequence 259, Application US/09978192A
: Patent No. US2002017753A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Deenoyers, Luc
: APPLICANT: Baton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gettisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
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: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kiljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paonl, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630Pic9

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62	PRIOR FILING DATE: 1998-04-01	62	PRIOR APPLICATION NUMBER: 60/084639
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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DB 141 VLSFTPRPDODHTDLCHVDFSRKGVSAQRTVRLRYAYAPRD 182
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QY 543 FQ 544
DB 543 FQ 544

RESULT 7
US-09-999-832A-259

Sequence 259, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999, 832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PROR APPLICATION NUMBER: 60/085697

Query Match 83.7% Score 2265; DB 10; Length 544;
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QY 253 -----PPENLRVWVSQANRYLE 270
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QY 271 NLGNGSLPYLEQOSLCVNTVHSSPPARLSMTQRCQVYSPSPDPGVLEPRVQVEH 330
Db 303 NLGNGSLPYLEQOSLCVNTVHSSPPARLSMTQRCQVYSPSPDPGVLEPRVQVEH 362
QY 331 GEFTCHARHPLGSOHSLSVHYKKGLISTAFSNGAFGIGTALLFCLALITKILP 390
Db 363 GEFTCHARHPLGSOHSLSVHYKKGLISTAFSNGAFGIGTALLFCLALITKILP 422
QY 391 KRRTQETPRPRSRSTIIDYINVVPTAGPLAKRNOKATPNSPRTPLPGAPSPESK 450
Db 423 KRRTQETPRPRSRSTIIDYINVVPTAGPLAKRNOKATPNSPRTPLPGAPSPESK 482
QY 451 NOKKOYQLSPFPKKSSTOAPESQESQELHVTLMFPGVRRPEARMKGTQADYAEV 510
Db 483 NOKKOYQLSPFPKKSSTOAPESQESQELHVTLMFPGVRRPEARMKGTQADYAEV 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 8
US-09-978-189-259
Sequence 259, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fond, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978, 189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-04-15

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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2, 3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSGQAMDGFWRVQESVWVPEGICISVPCSFSPYRQDWTGSTPAYGW 60
1 MLPLLLSLGSGQAMDGFWRVQESVWVPEGICISVPCSFSPYRQDWTGSTPAYGW 60
DB 1 MLPLLLSLGSGQAMDGFWRVQESVWVPEGICISVPCSFSPYRQDWTGSTPAYGW 60
QY 61 FKAFTETTKGAPATNHQSRREVEMSTRGRFOLTGDPKAGNCSLVIRDAQMODSQQYFFRV 120
61 FKAFTETTKGAPATNHQSRREVEMSTRGRFOLTGDPKAGNCSLVIRDAQMODSQQYFFRV 120
DB 61 FKAFTETTKGAPATNHQSRREVEMSTRGRFOLTGDPKAGNCSLVIRDAQMODSQQYFFRV 120
QY 121 ERGSYVRNFMNDGFELKVTALTOKPDVYI1PTELRQDPVYICVENMAFECCPPSFSW 180
121 ERGSYVRNFMNDGFELKVTALTOKPDVYI1PTELRQDPVYICVENMAFECCPPSFSW 180
DB 121 ERGSYVRNFMNDGFELKVTALTOKPDVYI1PTELRQDPVYICVENMAFECCPPSFSW 180
QY 181 TGAALSSQGTKPTTSHFVSFTPRRODHTDLTCHVDPSRKGVSAORVRLVAYAPRD 240
181 TGAALSSQGTKPTTSHFVSFTPRRODHTDLTCHVDPSRKGVSAORVRLVAYAPRD 240
DB 141 -----VLSTPRQDHTDLTCHVDPSRKGVSAORVRLVAYAPRD 182
241 LVISISRDNTPD-----PPENLRVWVSQANRTYLE 270
183 LVISISRDNTPALPEPQGNVPLYLBAQKQFLRLCAADSPPATLSWVLQNVLSSHP 242
QY 253 -----PPENLRVWVSQANRTYLE 270
243 WGPRLPLGLBPGYKADSGRYTCRAENRLGSOORALDLSVQYPPENLRVWVSQANRTYLE 302
DB 271 NLGNSTSLPYLEQOSLVCVTHSSPPARLSWTOGROGVSPSPGVELEPRVOYEHE 330
303 NLGNSTSLPYLEQOSLVCVTHSSPPARLSWTOGROGVSPSPGVELEPRVOYEHE 362
QY 331 GEFTCHARHPLGSOHVSLSLVHKKGLISTAFSNGAFILGITALLFLCLALIIKMLP 390
363 GEFTCHARHPLGSOHVSLSLVHKKGLISTAFSNGAFILGITALLFLCLALIIKMLP 422
DB 391 KRRTOTETPRPRSRSHSTIIDYINNVPTAGPLAQKRNQKTPMSPRTPLPGAPSPESKK 450
423 KRRTOTETPRPRSRSHSTIIDYINNVPTAGPLAQKRNQKTPMSPRTPLPGAPSPESKK 482
QY 451 NOKKQYOLPSPFPKSTOAPESQESOEELHYATLNPGRPPPEARMPGQADYAEVK 510
483 NOKKQYOLPSPFPKSTOAPESQESOEELHYATLNPGRPPPEARMPGQADYAEVK 542
DB 511 FQ 512
543 FQ 544

RESULT 9
US-09-978-608A-259
; Sequence 259, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

```

; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-259

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Query Match      83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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QY 1 MLPLLLSLGSGQAMDGREWIRVOESVMPPEGICISVCSFSYPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLGSGQAMDGREWIRVOESVMPPEGICISVCSFSYPRQDWTGSTPAYGYW 60
QY 61 FKAVETTTKGAQVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRY 120
DB 61 FKAVETTTKGAQVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRY 120
QY 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFNMAFECCPPPSFSW 180
DB 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFNMAFECCPPPSFSW 180
QY 181 TGAALSSGQKPTTSHSFSVLSFTPRQDHTDLTCHVDFSRKGVSAQRTVRLRAYAAPRD 240
DB 141 -----VLSFTPRQDHTDLTCHVDFSRKGVSAQRTVRLRAYAAPRD 182
QY 241 LVISISRDNTPD-----PPEMLRWVVSQANRTYLE 270
DB 183 LVISISRDNTPD-----PPEMLRWVVSQANRTYLE 270
QY 253 -----PPEMLRWVVSQANRTYLE 270
DB 243 WGPPELLELPYKAGDSGRYTCRAENRLSGQORALDLVQYPPENLRVWVSQANRTYLE 302
QY 271 NLNGSTSLPYLEGOSLCTVCTHSSPPARLSWTORQOVLSPSQSPGVLLEPRVOVEHE 330
DB 303 NLNGSTSLPYLEGOSLCTVCTHSSPPARLSWTORQOVLSPSQSPGVLLEPRVOVEHE 330
QY 331 GETTCAHAPLGSQVHSLSVHYKKGKLISTAFSNGAFIGITALLFTCLALLIMKTLIP 390
DB 363 GETTCAHAPLGSQVHSLSVHYKKGKLISTAFSNGAFIGITALLFTCLALLIMKTLIP 422
QY 391 KRTOETPRPRRSRSTILDYINVPYTAGPLAQKRNKAKATPNSPRTPLPGCAPSPESKK 450

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DB 423 KRTOETPRPRRSRSTILDYINVPYTAGPLAQKRNKAKATPNSPRTPLPGCAPSPESKK 482
QY 451 NOKKOYQLSPFEPKSSSTQAPESQSOEELHYATLNFQVRRPEARMKCTQADYAEVK 510
DB 483 NOKKOYQLSPFEPKSSSTQAPESQSOEELHYATLNFQVRRPEARMKCTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

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RESULT 10

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US-09-978-585A-259
; Sequence 259, Application US/0978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-259

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```

Query Match      83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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QY 1 MLPLLLSLGSGQAMDGREWIRVOESVMPPEGICISVCSFSYPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLGSGQAMDGREWIRVOESVMPPEGICISVCSFSYPRQDWTGSTPAYGYW 60
QY 61 FKAVETTTKGAQVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRY 120
DB 61 FKAVETTTKGAQVATNHOSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMODESQYFFRY 120
QY 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFNMAFECCPPPSFSW 180
DB 121 ERGSYVRYNFMNDGFFLKVTALQKPDVYIIPETLEPGQPVYICVFNMAFECCPPPSFSW 180

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QY 181 TGAALSSQGTKPTTSHSVLSFTPRPDHDTDLTCHVFSRKGVSAQRTVLRYAVAPRD 240
Db 141 -----VLSTPRPDHDTDLTCHVFSRKGVSAQRTVLRYAVAPRD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALEPOPOGNVYLAOKGOFRLRLCAADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVYVSAQNTVLE 270
Db 243 WGRPRGLLEPGKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVYVSAQNTVLE 302
QY 271 NLGNGTSLPYLEQSLCLVCTHSSPPARLSMTORGQVLSPPSPDGVLELPRVQYEHE 330
Db 303 NLGNGTSLPYLEQSLCLVCTHSSPPARLSMTORGQVLSPPSPDGVLELPRVQYEHE 362
QY 331 GERTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFGLGITALFLCLALIMKILP 390
Db 363 GERTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFGLGITALFLCLALIMKILP 422
QY 391 KRRTQETPPRRFSRSTIDYINVPYTAGPLAKRQKATPNSPRTPLPGAPSPESKK 450
Db 423 KRRTQETPPRRFSRSTIDYINVPYTAGPLAKRQKATPNSPRTPLPGAPSPESKK 482
QY 451 NQKKQYQLPSFPPEKSSQAPESQESQELHYATLNEPGVRRPPEARMPKGTQADYAEVK 510
Db 483 NQKKQYQLPSFPPEKSSQAPESQESQELHYATLNEPGVRRPPEARMPKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 11

US-09-978-191A-259
Sequence 259, Application US/09978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC4
CURRENT APPLICATION NUMBER: US/09/978.191A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-04-09

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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSGOAMDGRFMRVQESVWPEGLCTSPGSESYPRQDWTGTPATGYW 60
DB 1 MLPLLLSLGSGOAMDGRFMRVQESVWPEGLCTSPGSESYPRQDWTGTPATGYW 60
QY 61 FKAVETTKGAPVATNHOSEVEMSTRGRFQLTGDPKAGNCSLYIRDAQODESQYFFRV 120
DB 61 FKAVETTKGAPVATNHOSEVEMSTRGRFQLTGDPKAGNCSLYIRDAQODESQYFFRV 120
QY 121 ERGSVRYRNMNDGFEFLKYATLTKPKDVIYIPEITLBPQPYTVICVFMAFEBCPPSESW 180
DB 121 ERGSVRYRNMNDGFEFLKYATLTKPKDVIYIPEITLBPQPYTVICVFMAFEBCPPSESW 180
QY 181 TGAALSSQGTKPTTSHEFSVLETPRPODHTDLTCHVDFSRKGSYSAORTYRLRVAYAPRD 240
DB 141 -----VLSFTRPDQDHTMDLTCHVDFSRKGSYSAORTYRLRVAYAPRD 182
QY 241 LVISISRDNTPD----- 252
DB 183 LVISISRDNTPALPPOQGNVPYLEAQKGQFLRLCAADSPPATLSWVLQNRVLSSHP 242
QY 253 -----PPENLRVVSQANTVLE 270
DB 243 WGPRLGLLELPGYKAGDSGRYTCRAENRRLGSGQRAIDLISQYPPENLRVVSQANTVLE 302
QY 271 NLNGSTSLPYLEQSLCLVCVTHSSPPARLSWTQRQVILSPSQSDPGVLELPRVQVEHE 330
DB 303 NLNGSTSLPYLEQSLCLVCVTHSSPPARLSWTQRQVILSPSQSDPGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSOHSLSLSVHYKKGLISTAFSNGAFIGITALLFTCLALITMKILP 390
DB 363 GEFTCHARHPLGSOHSLSLSVHYKKGLISTAFSNGAFIGITALLFTCLALITMKILP 422
QY 391 KRRTQETPRPRFSRHSSTILDYINNVPTAGPLAOKRNQKATPNSPTPLPAPAPSPESK 450
DB 423 KRRTQETPRPRFSRHSSTILDYINNVPTAGPLAOKRNQKATPNSPTPLPAPAPSPESK 482
QY 451 NOKKOYOLSPFPKPSSTQAPESQSEELHATLTFPCVRRPRPEARMKGTQADYAEVK 510
DB 483 NOKKOYOLSPFPKPSSTQAPESQSEELHATLTFPCVRRPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 12
US-09-978-403A-259
; Sequence 259, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Query Match      83.7%  Score 2265;  DB 11;  Length 544;
Best Local Similarity 74.8%;  Pred. No. 2,3e-170;
Matches 450;  Conservative 1;  Mismatches 3;  Indels 148;  Gaps 2;

QY 1 MLPLLLSLGSGOAMDGFWIVQSVWVPEBLCTISVCSFSEYPRQDWTGSTPAYGW 60
DB 1 MLPLLLSLGSGOAMDGFWIVQSVWVPEBLCTISVCSFSEYPRQDWTGSTPAYGW 60
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DB 61 FKAUETTTGAPVATNHOSEVENSTGRFQLTGDPKAGKNCSLVIRAOQODESOYFRV 120
QY 121 ERGSIVRYNFMNDGFFLKTALNOKPDVYIPELTLEPGQPVTVICVFNMAREECPPEFSW 180
DB 121 ERGSIVRYNFMNDGFFLKTALNOKPDVYIPELTLEPGQPVTVICVFNMAREECPPEFSW 180
QY 181 TGAALSSGRTKPTTSHSFSVSEFPRQDHTDLDLCHVDFSRKGVSAQRTVRLAVAYAPRD 240
DB 141 -----VLSFPRQDHTDLDLCHVDFSRKGVSAQRTVRLAVAYAPRD 182
QY 241 LVISISDNTPD----- 252
DB 183 LVISISDNTPD----- 242
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QY 253 -----PENLRVMTSQANRYTLE 270
DB 243 WGPRLGLELPVKAKODSGRTYCRABENRLGSOQRALDLSVOYPPENLRVMTSQANRYTLE 302
QY 271 NINGSTSLPVEEGSLCLVCYTHSSPPARLSWTORGQVLSPOSPDPGVLELPVOYEHE 330
DB 303 NINGSTSLPVEEGSLCLVCYTHSSPPARLSWTORGQVLSPOSPDPGVLELPVOYEHE 362
QY 331 GEFTCHARNPLGSOHVSLSLVHYKKGLISAFSGARLGGITALLFLCLALIMKILP 390
DB 363 GEFTCHARNPLGSOHVSLSLVHYKKGLISAFSGARLGGITALLFLCLALIMKILP 422
QY 391 KRRTQETPRPRFSRHSHTILDYINVPYAGPLAQRKRNKATPNSPRTPPPGAPSPSK 450
DB 423 KRRTQETPRPRFSRHSHTILDYINVPYAGPLAQRKRNKATPNSPRTPPPGAPSPSK 482
QY 451 NOKKOYOLPSPPEKSSTOAPEOSQOEELHYATLNEPGVPRPEARMKGTQADYAEVK 510
DB 483 NOKKOYOLPSPPEKSSTOAPEOSQOEELHYATLNEPGVPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 13
US-09-978-564A-259
; Sequence 259, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978, 564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2.3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLSLILGSGAMDRFWIRVOESVMEPEGICISVCSFSYPRDMDGSTPYAGW 60
DB 1 MLPLLSLILGSGAMDRFWIRVOESVMEPEGICISVCSFSYPRDMDGSTPYAGW 60
QY 61 FRAVETTKGAPVATNHOSREVEEMSTRGRFOLTGDPKNGSLVIRDAQMODESQYFRV 120
DB 61 FRAVETTKGAPVATNHOSREVEEMSTRGRFOLTGDPKNGSLVIRDAQMODESQYFRV 120
QY 121 ERGSVYRNEMNDGFEFLVLTALQKRDVYIPELPEGQPYVICVFNNAFEECPPEFSW 180
DB 121 ERGSVYRNEMNDGFEFLVLTALQKRDVYIPELPEGQPYVICVFNNAFEECPPEFSW 180
QY 181 TGAALSSOGTKPTTSHFSVLSFTPRPDHDTLCTCHVDPSRKVSAQRTVRLRVAYARD 240
DB 181 TGAALSSOGTKPTTSHFSVLSFTPRPDHDTLCTCHVDPSRKVSAQRTVRLRVAYARD 240
QY 141 -----VLSETPRPDNDHNDLCHVDFSRKGVSAQRTVRLRVAYARD 182
DB 141 -----VLSETPRPDNDHNDLCHVDFSRKGVSAQRTVRLRVAYARD 182
QY 241 LVISIRNDTP----- 252
DB 241 LVISIRNDTP----- 252
QY 183 LVISIRNDTPALEPQGNVPLEAKGQFLRLCAADSOPTATLSWLNRYLSSHP 242
DB 183 LVISIRNDTPALEPQGNVPLEAKGQFLRLCAADSOPTATLSWLNRYLSSHP 242
QY 253 -----PENLAVMSQANRYTLE 270
DB 253 -----PENLAVMSQANRYTLE 270
QY 243 WGPRLGLELPGVAKAGDSGRITTCRAENLRSQORALDISVQYPPENLAVMSQANRYTLE 302
DB 243 WGPRLGLELPGVAKAGDSGRITTCRAENLRSQORALDISVQYPPENLAVMSQANRYTLE 302
QY 271 NLGNGTSLPVLGSGSLVCVTHSSPPARLSWTOGVOVLSPOSDPGLVLEPRVOEHE 330
DB 271 NLGNGTSLPVLGSGSLVCVTHSSPPARLSWTOGVOVLSPOSDPGLVLEPRVOEHE 330
QY 303 NLGNGTSLPVLGSGSLVCVTHSSPPARLSWTOGVOVLSPOSDPGLVLEPRVOEHE 362
DB 303 NLGNGTSLPVLGSGSLVCVTHSSPPARLSWTOGVOVLSPOSDPGLVLEPRVOEHE 362
QY 331 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFGLGICITALLFLCALITIMILP 390
DB 331 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFGLGICITALLFLCALITIMILP 390
QY 363 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFGLGICITALLFLCALITIMILP 422
DB 363 GEFCHAHRLPGSHVSLSVHKKGLISTAFSNGAFGLGICITALLFLCALITIMILP 422
QY 391 KRRTQETPRPRFSRHSITLDYINVVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKK 450
DB 391 KRRTQETPRPRFSRHSITLDYINVVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKK 450
QY 423 KRRTQETPRPRFSRHSITLDYINVVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKK 482
DB 423 KRRTQETPRPRFSRHSITLDYINVVPTAGPLAOKRNOKATPNSPRTPLPGAPSPESKK 482
QY 451 NOKROYOLPSFPEPKSSTQAPESQSEELHYATLNFPGVPRPEARMPKGTQADYAEVK 510
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QY 483 NOKROYOLPSFPEPKSSTQAPESQSEELHYATLNFPGVPRPEARMPKGTQADYAEVK 542
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QY 511 FQ 512
DB 511 FQ 512
QY 543 FQ 544
DB 543 FQ 544

RESULT 14
US-09-999-833A-259
; Sequence 259, Application US/09999833A
; Publication No. US20030034405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjaevn, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999, 833A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 83.7% Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;
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Db 61 FKAVTETTKGAPATNHSREVENSTGRGROLTGDPKKGKCSLITRAQMODSQQYFRV 120
QY 121 ERGSYVYRPNMNGGFLKVTALTOKPDVYIPEFLPEQPTVICFNNAREECPPEFSW 180
Db 121 ERGSYVYRPNMNGGFLKVTALTOKPDVYIPEFLPEQPTVICFNNAREECPPEFSW 180
QY 181 TGAALSSQGTPTTSHFSVLSFTTPRQDHDITLCHVDSRKGVSAQRTVRLRAYAPRD 240
Db 181 TGAALSSQGTPTTSHFSVLSFTTPRQDHDITLCHVDSRKGVSAQRTVRLRAYAPRD 240
QY 141 -----VLSFTTPRQDHDITLCHVDSRKGVSAQRTVRLRAYAPRD 182
Db 141 -----VLSFTTPRQDHDITLCHVDSRKGVSAQRTVRLRAYAPRD 182
QY 241 LVTSISRDNTPD----- 252
Db 241 LVTSISRDNTPD----- 252
QY 183 LVTSISRDNTPDLEPOQGNVYVLEACKGQFLRLCAADSOPTATLSWLVONRVLSSSH 242
Db 183 LVTSISRDNTPDLEPOQGNVYVLEACKGQFLRLCAADSOPTATLSWLVONRVLSSSH 242
QY 253 -----PPENLRVWVSQANRTVLE 270
Db 243 WGPRLPLGLBPGVKAGDSGRYTCRAENRLSQQRALDLSVOYPPENLRVWVSQANRTVLE 302
QY 271 NLGNGTSLPVLEGSQCLVCVTTHSSPARLSWTORGCVLSPSQPSDFGVLELPRVOYHE 330
Db 271 NLGNGTSLPVLEGSQCLVCVTTHSSPARLSWTORGCVLSPSQPSDFGVLELPRVOYHE 330

Db 303 NMGNTSLPYLEQSLCLVGVTHSSPPARLSWTORGQVISPSPDPGVLELPVQVEHE 362
QY 331 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFIGITALLFLIALIINKIIP 390
Db 363 GEFTCHARHPLGSOHVSLSVHYKKGLISTAFSNGAFIGITALLFLIALIINKIIP 422
QY 391 KRRTQETPRPRRSRSTIIDYINVPVPLAQKRNQKATPNSPTPLPGAPSPESK 450
Db 423 KRRTQETPRPRRSRSTIIDYINVPVPLAQKRNQKATPNSPTPLPGAPSPESK 482
QY 451 NOKKOQLPSPFPKSTAPESQESQELHTATLTFPGVRRPRPEARMKGTQADYAEVK 510
Db 483 NOKKOQLPSPFPKSTAPESQESQELHTATLTFPGVRRPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

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Publication No. US20030054986A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerder, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C12
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; PRIOR FILING DATE: 1998-05-15
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Query Match      83.7%; Score 2265; DB 11; Length 544;
Best Local Similarity 74.8%; Pred. No. 2,3e-170;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY      1 MLLPLLSLGGSGAMDRFWIRVOESVWVEGLCTISVCSFSYPRDWTGSTPAYGYW 60
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DB      1 MLLPLLSLGGSGAMDRFWIRVOESVWVEGLCTISVCSFSYPRDWTGSTPAYGYW 60
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QY      61 FRAVETTTGAPVATNHQSEVEMSTRGRFQLTGPAPKNCSLVIRDAQMOESQYFFRV 120
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DB      61 FRAVETTTGAPVATNHQSEVEMSTRGRFQLTGPAPKNCSLVIRDAQMOESQYFFRV 120
        |||||||

QY      121 ERGSYVRVFMNDGFFLKVTALTQKPDVYIPELTBEGQVYVICVFNMAFECCPPPSFW 180
        |||||||
DB      121 ERGSYVTVFMNDGFFLKVT----- 140

QY      181 TGAALSSQGTKPTTSHFSVLTPTPRPDHDTLCTCHVDSRKGVSAQRTVRLRVAVAPRD 240
        |||||||
DB      141 -----VLSFTPRPDHDTLCTCHVDSRKGVSAQRTVRLRVAVAPRD 182

QY      241 LVYSISRDNTPD----- 252
        |||||||
DB      183 LVYSISRDNTPALPEPQGNVPLYLEAQKQFLRLCAADSQPPATLSWVLQNRVLSSHP 242

QY      253 -----PPENLRVWVSQANRTVLE 270
        |||||||
DB      243 MGPRPLGLELPGVKAAGDSGRYTCRAENRLSGOORALDLSVQYPPENLRVWVSQANRTVLE 302
        |||||||

QY      271 NLGNGTSLPYLEGOSLCTVCVTHSSPPARLSTORGQVLSPOSPDPGLLELPRVOVEHE 330
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DB      303 NLGNGTSLPYLEGOSLCTVCVTHSSPPARLSTORGQVLSPOSPDPGLLELPRVOVEHE 362

QY      331 GEFTCHARPPLGSOHVSLSLSVHYKKGLISTAFSNGAFIGITALLLFLCLALLIIMKILP 390
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DB      363 GEFTCHARPPLGSOHVSLSLSVHYKKGLISTAFSNGAFIGITALLLFLCLALLIIMKILP 422

QY      391 KRRTQETPRPRPSRSTILLDYINVPTAGPLAQRNOKATNSPRTPLPPGAPSPESK 450
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DB      423 KRRTQETPRPRPSRSTILLDYINVPTAGPLAQRNOKATNSPRTPPGAPSPESK 482

QY      451 NOKKOYQLPSPEPKSSTQAPESQSEELHATLNFPGVRRPPEARMPKGTQADYAEVK 510
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DB      483 NOKKOYQLPSPEPKSSTQAPESQSEELHATLNFPGVRRPPEARMPKGTQADYAEVK 542

QY      511 FQ 512
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DB      543 FQ 544

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Search completed: October 8, 2003, 20:05:39
 Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:03:42 : Search time 5699 Seconds -
(without alignments)
3675.334 Million cell updates/sec

Title: US-09-937-636-3

Sequence: 1 MLPLLSLLGSGQAMDGR.....REPARMKGTQADYAEVKFQ 512

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+pn.model -DRV=ylh
-Q/cg22.1/USPTO.spool/US09937636/runat.08102003-083236-29962/app.query.fasta_1.711
-DB=GenEmbl -QMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09937636.ecgn.1.1.3635.runat.08102003.083236.29962 -NCPU=6 -ICPU=3
-NC_MAP -LARGEOURER -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
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41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2615	96.6	3124	9 AF311905	AF311905 Homo sapi
2	2580.5	95.4	2208	6 AX365530	AX365530 Sequence
3	2580.5	95.4	3012	9 AF301007	AF301007 Homo sapi
4	2580.5	95.4	3024	6 AX365542	AX365542 Sequence
5	2576.5	95.2	2176	9 AF310233	AF310233 Homo sapi
6	2278	84.2	2565	6 AX365516	AX365516 Sequence
7	2265	83.7	2764	6 AX376050	AX376050 Sequence
8	2220.5	82.1	3099	6 BD011516	BD011516 Sequence
9	2220.5	82.1	3099	6 BD011517	BD011517 Sequence
10	2196.5	81.2	2126	6 AY032685	AY032685 Homo sapi
11	2142.5	79.2	2231	6 AX365517	AX365517 Sequence
12	1960	72.4	2321	6 AX497858	AX497858 Sequence
13	1929.5	71.3	2823	6 AX365518	AX365518 Sequence
14	1824	67.4	2529	6 AX365544	AX365544 Sequence
15	1728	62.1	1665	6 AX365519	AX365519 Sequence
16	1680.5	62.1	2154	6 AX430336	AX430336 Sequence
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19	1646.5	60.8	195993	2 AC014953	AC014953 Homo sapi
20	1513.5	55.9	3183	9 AF337818	AF337818 Homo sapi
21	1503.5	55.6	2273	9 AB072038	AB072038 Homo sapi
22	1454.5	53.8	2052	6 AX365546	AX365546 Sequence
23	1389.5	51.3	2605	6 BC039008	BC039008 Homo sapi
24	1366	50.5	17216	2 AC130272	AC130272 Homo sapi
25	1343.5	49.6	2067	10 AY210400	AY210400 Mus muscu
26	1337	49.4	167266	2 AC130273	AC130273 Homo sapi
27	1303	48.2	2190	9 BC009955	BC009955 Homo sapi
28	1160.5	42.9	146741	9 AC011452	AC011452 Homo sapi
29	1144	42.3	175999	2 AC021154	AC021154 Homo sapi
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35	909	33.6	2121	9 AK095919	AK095919 Homo sapi
36	909	33.6	2180	9 BC035809	BC035809 Homo sapi
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40	888	32.8	1597	6 E40809	E40809 Sequence
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RESULT 1

ALIGNMENTS

AF311905 3124 bp mRNA linear PRI 21-AUG-2001
 LOCUS Homo sapiens sialic acid-binding Ig-like lectin 10 (SIGLEC10) mRNA.
 DEFINITION complete cds.
 ACCESSION AF311905
 VERSION AF311905.1 GI:15217165
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 3124)
 AUTHORS Li, N., Zhang, W., Wan, T., Zhang, J., Chen, T., Yu, Y., Wang, J. and
 Cao, X.
 TITLE Cloning and characterization of Siglec-10, a novel sialic acid
 binding member of the Ig superfamily, from human dendritic cells
 JOURNAL J. Biol. Chem. 276 (30), 28106-28112 (2001)
 MEDLINE 21359381
 PUBMED 11358961
 REFERENCE 2 (bases 1 to 3124)
 AUTHORS Li, N., Zhang, W., Wan, T. and Cao, X.
 TITLE Direct submission
 JOURNAL Submitted (15-AUG-2001) Department of Immunology, Second Military
 Medical University, 800 Xiangyin Rd., Shanghai 200433, P.R.China
 FEATURES
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 Percent Similarity: 84.39% Conservative: 2
 Best Local Similarity: 84.05% Mismatches: 4
 Query Match: 96.64% Indels: 90
 DB: 9 Gaps: 1
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RESULT 2

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 LOCUS AX365530
 DEFINITION Sequence 15 from Patent WO0208257.
 ACCESSION AX365530
 VERSION AX365530.1 GI:18697092
 KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Longphre, M., Chang, H. and Whitney, G.
 Novel siglecs and uses thereof
 Patent: WO 0208257-A 15 31-JAN-2002;
 BRISTOL-MYERS SQUIBB COMPANY (US)
 location/Qualifiers

FEATURES

source

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BASE COUNT 463 a 737 c 604 g 404 t
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 Score: 2580.50 Matches: 510
 Percent Similarity: 73.31% Conservative: 1
 Best Local Similarity: 95.17% Mismatches: 185
 Query Match: 6 Gaps: 2

US-09-937-636-3 (1-512) x AX365530 (1-2208)

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RESULT 3			
LOCUS	AF301007	3012 bp	mRNA linear PRI 26-JUL-2002
DEFINITION	Homo sapiens stialic acid-binding immunogloblin-like lectin 10 (StigLEC10) mRNA, complete cds.		

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DEFINITION Sequence 27 from Patent WO0208257.
ACCESSION AX365542
VERSION AX365542.1 GI:18697098
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Longphre, M., Chang, H. and Whitney, G.
TITLE Novel siglecs and uses thereof
JOURNAL Patent: WO 0208257-A 27 31-JAN-2002;
BRIEF-ABSTRACT BISTROL-MYERS SQUIBB COMPANY (US)
FEATURES
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Qy	496	AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln	512
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DEFINITION	Homo sapiens stalleic acid binding immunoglobulin-like lectin 10 (SIGLEC10) mRNA, complete cds.		
ACCESSION	AF310233		
VERSION	AF310233.1	GI:14164612	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2176)		
AUTHORS	Munday,J., Kerr,S., Ni,J., Cornish,A.L., Zhang,J.Q., Nicoll,G., Floyd,H., Mettel,M.-G., Moore,P., Liu,D. and Crocker,P.R.		
TITLE	Identification, characterization and leucocyte expression of Siglec-10, a novel human stalleic acid-binding receptor		
JOURNAL	Biochem. J. 355 (Pt 2), 489-497 (2001)		
MEDLINE	21181584		
PUBMED	11284738		
REFERENCE	2 (bases 1 to 2176)		
AUTHORS	Cornish,A.L., Ni,J. and Crocker,P.R.		
TITLE	Submitted (02-OCT-2000) School of Biological Sciences, University of Dundee, Dow Street, Dundee DD6 8AT, Scotland, United Kingdom		
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DB	398 GAGAGAGGAACTATGTAGATATATATTATCAATGAACGATGGGTTCTTTCTAAAGTAAACA	457	
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AX365516
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ACCESSION  AX365516
VERSION     AX365516.1  GI:18697085
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REFERENCE  1
            Longpre, M., Chang, H. and Whitney, G.
            Novel singlec and uses thereof
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            BRISTOL-MYERS SQUIBB COMPANY (US)
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Db      |||||||
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LOCUS AX376050
DEFINITION Sequence 117 from Patent WO0168848.
ACCESSION AX376050
VERSION AX376050.1 GI:19170417
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Baker, K. P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P. J.,
Gurney, A. L., Pan, J., Smith, V., Watanabe, C. K., Wood, W. I. and
Zhang, Z.
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patent: WO 0168848-A 117 20-SEP-2001;
Genentech, Inc. (US)
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DEFINITION Sialoadhesin family 4(SAF-4) cDNA.
ACCESSION BD011516
VERSION BD011516.1 GI:18639889
KEYWORDS JP 2001502359-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3099)
AUTHORS Kikly,K.K. and Miller,C.L.E.
TITLE Sialoadhesin family 4(SAF-4) cDNA
PATENT: JP 2001502359-A 1 20-FEB-2001;
JOURNAL SMITHKLINE BEECHAM CORP
COMMENT OS Homo sapiens (human)
PN JP 2001502359-A/1
PD 20-FEB-2001
PF 27-MAY-1998 JP 1999500864
PR 27-MAY-1997 US 60/047572
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A61K38/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705, PC
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LOCUS S140adhesin family 4(SAF-4) cDNA.
DEFINITION BD011517
ACCESSION BD011517.1 GI:18639890
VERSION JP 2001502359-A/2.
KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 3099)
AUTHORS	KIKLY/K.R. and MILLER,C.L.E.
TITLE	Sialoadhesin family 4(SAF-4) cDNA
JOURNAL	Patent: JP 2001502359-A 2 20-FEB-2001;
COMMENT	SMITHKLINE BEECHAM CORP OS Homo sapiens (human) PN JP 2001502359-A/2 PD 20-FEB-2001 PF 27-MAY-1998 JP 1999500864 PR 27-MAY-1997 US 60/047572 PI KRISTINE KAY KIKLY,CONNIE LYNN ERICKSON MILLER PC A61K36/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705,PC C07K16/00, PC C07K16/18,C07K16/28,C12N15/01,C12N15/11,C12N15/12,C12N15/63 CC
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Score:	2220.50 Matches: 452
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Best Local Similarity:	64.85% Mismatch: 1
Query Match:	82.06% Indels: 243
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QY	21 PheTrpIleaValGInGInuSeVaIMetVaIProGluGlyLeuCysILeserValPro 40
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DEFINITION	Homo sapiens stailic acid-binding protein splice variant 3.
ACCESSION	AY032685
VERSION	AY032685.1
KEYWORDS	GI:20384701
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Kltzli,F., Martinez-Barriocanal,A., Lopez-Botet,M. and Sayos,J.
TITLE	Cloning of two new splice variants of Stiglec-10 and mapping of the interaction between Stiglec-10 and SHP-1
JOURNAL	Biochem. Biophys. Res. Commun. 296, 355-362 (2002)
REFERENCE	2 (bases 1 to 2126)
AUTHORS	Kltzli,F., Alvarez-Erillo,D., Sayos,J. and Lopez-Botet,M.
TITLE	Direct Submission
JOURNAL	Submitted (17-APR-2001) Immunology, Universitat Pompeu Fabra (CEXS), Dr. Aiguader No. 80, Barcelona 08003, Spain
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 LOCUS AX365517
 DEFINITION Sequence 2 from Patent WO0208257.
 ACCESSION AX365517
 VERSION AX365517.1 GI:18697086
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Longpre, M., Chang, H. and Whitney, G.
 Novel siglecs and uses thereof
 Patent: WO 0208257-A 2 31-JAN-2002;
 BRISTOL-MYERS SQUIBB COMPANY (US)
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 QY 58 GlyTyrTrpPheLysAlaValIleThrGluThrThrLysGlyAlaProValAlaTrpAsnHis 77
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QY      308 Val1LeuSerProSerGlnProSerAspProGlyVal1LeuGluLeuProArgVal1GlnAl 327
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QY      328 GlnHisGlyGlyLeuPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSer 347
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QY      348 LeuSerLeuSerVal1HisTyf----- 354
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QY      373 1IleThrAlaLeuLeuPheLeuCysLeuAlaLeu1Ile1IleMetLys1IleLeuProLysArg 392
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QY      493 ArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyfArgLysVal1LysPheGln 512
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ACCESSION      AX497858
VERSION      AX497858.1 GI:23342965
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Baughn,M.R., Lu,D.A., Yue,H., Elliott,V.S., Thangavelu,K., Ramkumar,J., Lu,Y., Lo,T.P., Gururajan,R., Gandhi,A.R., Arvizu,C. and Yao,M.G.
TITLE      Immunoglobulin superfamily proteins
JOURNAL      Patent: WO 0240671-A 8 23-MAY-2002;
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Db	252	ACGCCGACACCCGACGACCAACACGCACTCCACTCTGATGTGGACTTCTCCGAAG	311
OY	223	GlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProAlaAspLeuVal	242
Db	312	GGTGTGACCGTCACAGAGAGACCGTCCGACTCCGTGTGGCTATGGCCCCACAGACCTTGT	371
OY	243	IleSerIleSerArgAspAsnThrProAsp	252
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OY	252	-----	252
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Db	672	CCTCAGAGAACTCGAGAGTATGTGTTCCCAAGCAACAGACAGTCTTGAAAACTT	731
OY	273	GlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerIleuCysValAlaThr	292
Db	732	GGGAACGGCACGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTGATGTACAA	791
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OY	398	ThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnValPro	417
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OY	418	ThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThr	437
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OY	438	ProLeuProGlyAlaLysProSerProGluSerLysLysAsnGlnLysGlnTyrGln	457
Db	1512	CCTCTTCCACACAGGTGCTCTCTCCCGAATCAAGAGAACCGAAGAAAGCACTATCAG	1571
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OY	498	MetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln	512
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REFERENCE	synthetic construct		
AUTHORS	artificial sequences.		
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JOURNAL	Longphre,M., Chang,H. and Whitney,G. Novel sigleics and uses thereof Patent: WO 0208257-A 29 31-JAN-2002; BRISTOL-MYERS SQUIBB COMPANY (US)		
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Db	189	TTTCGTGATACGAGTCCAGAGCATCATGATGATGTCGGAGGCGCTGTGCATCTCTTGCCC	248

QY	4	CysSerPheSerThrProArgLysProPheLysSerThrProAlaTyrGlyTyrTrp	60
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QY	61	PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	80
Db	309	TTCAAGCAGTAGTACTGAGACCAACCAAGGGTGTCTCTGTGGCCACAAACCAACGAGTGTGA	368
QY	81	GluValGlnMetSerThrArgGlyLysArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	100
Db	369	GAGGTGGAAATAGACACCGGGGGCGATTCACGTCACCTGGGGGATCCGGCAAGGGAGAC	428
QY	101	CysSerLeuValLLeArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal	120
Db	429	TGCTCCTTGATGATCAGAGACGCGAGATGCGATGATGATCACTACTCTTTGGGGTG	488
QY	121	GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr	140
Db	489	GAGAGAGGAGCTATGATGATATATTTCAAGAACGATGGGTTCTTTCTAAAGTACA	548
QY	141	AlaLeuThrGlnLysProAspValTyrLLeProGluThrLeuGlnProGlyGlnProVal	160
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QY	161	ThrValLLeCysValPheAsnTrpAlaPheGlnGlyCysProProSerPheSerTrp	180
Db	609	ACGGTCATCTGTGTGTTTAACGGGCGCTTGGAGATGTCCACCCCTTCTTCTCTGG	668
QY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu	200
Db	669	ACGGGGGCTGCCCTTCTCTCCCAAGAACCAACCAACGACCTCCCACTTCTCACTGTCTC	728
QY	201	SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	220
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QY	221	ArgLysGlyValSerAlaGlnArgThrValArgLeuAlaTyrAlaProArgAsp	240
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QY	291	ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	310
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QY	311	ProserGlnProSerAspProGlyValLeuGlnLeuProArgValAlnValGlnHisLeu	330
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QY	403	PheSerArgHisSerThrIleLeuAspTyrIleAsnValAlaPro---ThrAlaGlyPro	421
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Db	1676	CCTCAGGCTCCGCTGTGAGGCCCTGAGACGTCCATGGGGCCAGAGTGA-----1724	
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REFERENCE			
AUTHORS	1 Longphire, M., Chang, H. and Whitney, G.		
TITLE	Novel styles and uses thereof		
JOURNAL	Patent: WO 0208257-A 4 31-JAN-2002;		
	BRISTOL-MYERS SQUIBB COMPANY (US)		
FEATURES	Location/Qualifiers		
SOURCE	1..1665		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		

BASE COUNT	433 a	476 c	440 g	316 t
ORIGIN				

Alignment Scores:

Pred. No.:	3.07e-92	Length:	1665
Score:	1728.00	Matches:	336

US-09-937-636-3 (1-512) x AX365519 (1-1665)

Oy	4	ProArgGlnAspTrpThrGlySerThrProAlaArgGlyTrpTrpPheLysAlaValThr	65
Db	2	CCCGGCAAGACTGGACAGGGCTCTACCCCACTTATGGCTACTGTTCAAGCAGTACT	61
Oy	66	GluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArgGluValGluMetSer	85
Db	62	GAGACACCAAGGGTCTCTTGCGCCCAAAACCAACGAGATCGAAGGTGGAAATGAGC	121
Oy	86	ThrArgGlyArgPheGlnLeuThrGlnLysProAlaLysGlyAsnCysSerLeuValIle	105
Db	122	ACCGGGGCGCATTCAGCTCAGCTGGGATCCCGCAAGGGGAATCTCTCTGGTGATC	181
Oy	106	ArgAspAlaGlnMetGlnAspGluSerGlnTrpPhePheArgValGluArgGlySerTyr	125
Db	182	AGAGACGCGCAGATGCAGGATGAGTCACAGTACTCTTCTGGGTGGAGAGAGAACTAT	241
Oy	126	ValArgTyrAsnPheMetAsnAspLysPhePheLeuLysValThrAlaLeuThrGlnLys	145
Db	242	GTGAGTAAATTAATTCATGACAGTGGTCTTTCTTAAAGTACAGCCCTGACACAG	301
Oy	146	ProAspValTyrTrlSerGlnLysLeuLysProGlyGlnProValThrValIleCysVal	165
Db	302	CGTGAATGTACATCCCGAGACCTGTGAGCCCGGCGACCGGTGAGGTCACTGTGTG	361
Oy	166	PheAsnTrpAlaPheGlnGluCysProProPheSerPheSerTrpThrGlyAlaAlaLeu	185
Db	362	TTTAACTGGGCTTTGAGAAATGTCACCCCTTTCTCTGAGCGGGGCGTCCCTC	421
Oy	186	SerSerGlnGlyThrLysProThrTrpSerHisPheSerValIleAspPheThrProArg	205
Db	422	TCTCCCAAGAGAACCAACCAACGACCTCCCACTTCTCAGTGTCTCAAGTCTCAGCC	481
Oy	206	ProGlnAspHisAspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSer	225
Db	482	CCCAAGAGACCAACACGACCTCAGCTGCGCATGGAGCTTCACAGAAAGGCGTGAAC	541
Oy	226	AlaGlnArgThrValArgLeuArgValAlaIleTyrAlaProAlaGspLeuValIleSerIle	245
Db	542	GTAACAGAGACCTGCGACTCGTGGCTGATGCCCCCAAGACCTGTGTATCAGCATT	601
Oy	246	SerArgAspAsnThrProAsp	252
Db	602	TTCACGTGACACACACGACGACCTGTGAGGCCACAGGCCCAAGGAATGTCCATACTCGAA	661
Oy	252	-----	252
Db	662	GCCCAAAAAGCCAGTCTCGCGGCTCCTGTGTGCTGTGACAGCAGCCCGCTCCACA	721
Oy	252	-----	252
Db	722	CTGACGTGGGTCTCTGACAGACAGAGTCTCTCTCTGCTCCATCTCCCTGGGGCCCTAGACC	781
Oy	252	-----	252
Db	782	CTGGGCTGGAGCTGCCGGGTGAAGGCTGGGATTCAGGGCTGACACTGCGAGCG	841
Oy	253	-----	253
Db	842	GAGACAGGCTTGCTCCCGACGAGGACCTTGAGACTCTGTGTGACATATCTTCACAG	901

[illegible]

Search completed: October 8, 2003, 21:48:29
Job time : 5749 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:03:17 ; Search time 408 Seconds
(without alignments)
3387.530 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq_19Jun03:*

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- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2706	100.0	1536	21	AAA37847	Human obesity prot
2	2580.5	95.4	2208	24	ABK43367	DNA encoding stail
3	2580.5	95.4	3024	24	ABK43373	DNA encoding stail
4	2278	84.2	2365	24	ABK43360	DNA encoding stail
5	2265	83.7	2764	20	AAZ34109	Human PRO940 nucle
6	2265	83.7	2764	21	AACT8510	Human PRO940 (UNQ4
7	2265	83.7	2764	22	ACA55983	Human DNA encoding
8	2265	83.7	2764	25	ACAS7741	Human PRO940 cdna.
9	2265	83.7	2764	25	ABX98211	Human CDNA encodin
10	2265	83.7	2764	25	ABX98713	Novel human secret
11	2265	83.7	2764	25	ACA05758	Human secreted/tira
12	2265	83.7	2764	25	ABX92481	CDNA encoding huma
13	2265	83.7	2764	25	ABX97802	Human PRO polynuc
14	2265	83.7	2764	25	ABX78586	Human PRO polynuc
15	2265	83.7	2764	25	ABX75599	Human CDNA encodin
16	2265	83.7	2764	25	ABX76804	Human PRO polynuc
17	2265	83.7	2764	25	ABX16644	Human CDNA encodin
18	2220.5	82.1	1917	21	AAA37848	Human obesity prot
19	2220.5	82.1	3099	20	AAV99911	Human staloadesin
20	2220.5	82.1	3099	20	AAV99912	Human staloadesin
21	2197.5	81.2	2295	21	AAA80610	Human CD33-like se
22	2142.5	79.2	2954	24	ABK43361	DNA encoding stail
23	2142.5	79.2	2954	24	ABK43361	DNA encoding stail
24	1929.5	71.3	2823	24	ABK43362	DNA encoding stail
25	1824	67.4	2529	24	ABK43374	Siglec-BMS-13a-hig
26	1728	62.1	1665	24	ABK43363	DNA encoding stail
27	1680.5	62.1	2154	24	ABO72566	Human MDR1 encodin
28	1533.5	56.7	1029	23	AA580254	DNA encoding novel
29	1513.5	55.9	2061	24	ABO86144	Novel human gene.
30	1507.5	55.7	2058	25	ABO53168	Human Siglec-12 DN
31	1454.5	53.8	2052	24	ABK43375	Siglec-BMS-13a-hig
32	1443	53.3	2004	24	ABO86145	Novel human gene.
33	1396.5	51.6	1344	21	AAA80619	Human secreted pro
34	1336	49.4	1974	23	AA580252	DNA encoding novel
35	1329	49.1	1859	23	AA584407	DNA encoding novel
36	1270.5	47.0	1578	23	AA580253	DNA encoding novel
37	947	35.0	1592	24	AA38935	Siglec-L coding c
38	924	34.1	1473	24	ABA90353	Human polynucleoti
39	916	33.9	1736	24	ABD37892	Siglec-like gene (
40	916	33.9	1860	24	ABA90352	Human polynucleoti
41	909	33.6	1987	22	AAO08641	Human kinase (PKIN
42	909	33.6	2139	22	AAE76851	Human secreted pro
43	900	33.3	1554	24	ABK43364	DNA encoding stail
44	888	32.8	1597	20	AAK17773	SAF-2 polypeptide
45	888	32.8	2900	20	AAK17772	SAF-2 polypeptide

ALIGNMENTS

with offiation

RESULT 1
ID AAA37847 standard; DNA: 1536 BP.
AC AAA37847;
XX
XX 12-FEB-2001 (first entry)
DE Human obesity protein binding protein-2 homologue coding sequence #1.
XX
XX Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
KW obesity-related disorder; therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX
XX Key Location/Qualifiers
FH 1..1536
FT CDS

FT /tag= a
FT /product= hOB-BP2h
XX MO200059942-A2.
XX 12-OCT-2000.
XX 22-MAR-2000; 2000WO-US06682.
XX 02-APR-1999; 99US-0127667.
XX (ELIL) LILLY & CO ELI.
XX Su EW, Wei J;
XX WPI: 2000-664992/64.
XX P-PSDB; AAY97542.
XX
XX New human obesity protein binding protein-2 homologue nucleic acids,
XX polynucleotides and polypeptides useful for producing medicament for
XX treating obesity and/or obesity-related disorders
XX
XX Claim 3; Page 85; 92pp; English.

XX This sequence encodes a human obesity protein binding protein-2 homologue
XX (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides
XX may be used for the manufacture of a medicament for the treatment of
XX obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are
XX useful as probes or amplification primers in the detection,
XX quantification or isolation of gene sequences or transcripts, for
XX recombinant expression of hOB-BP2h polypeptides, as immunogens in the
XX preparation and screening of antibodies, and in sense or antisense
XX suppression of one or more hOB-BP2h genes or nucleic acids, host cell
XX or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and
XX polypeptides are useful for raising or screening antibodies that
XX specifically binds to the hOB-BP2h polypeptides.

XX Sequence 1536 BP; 354 A; 487 C; 401 G; 294 T; 0 other;

Alignment Scores:

Score: 2,47e-185 Length: 1536
Percent Similarity: 2706.00 Matches: 512
Best local Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
DB: 21 Indels: 0 Gaps: 0

US-09-937-636-3 (1-512) x AAA37847 (1-1536)

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DB 1 ATGCTACTGACGACGCTGCTCTCTCGTGGTGGGGGTCCAGGCAATGAGTGGAGA 60
QY 21 PheTrpIleArgValGlnGlnSerValMetValProGlnGlyLeuCysIleSerValPro 40
DB 61 TTCTGAGATACGACGAGAGAGTCACTGATGGTGGCGGAGGCTGTGCATCTCTGTGCC 120
QY 41 CysSerPheSerTyrrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60
DB 121 TGTCTTCTCTCTACCCCGACAGAGCTGACAGAGGTATACCCGCTTAATGCTACTGG 180
QY 61 PheIysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
DB 181 TTCAAAGCAGTACGACGACACCAACCAAGGCTGCTCTGGCCACAAACACACAGAGTGA 240
QY 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
DB 241 GAGGTGGAATGAGACCCGGGGCGGATTCACAGCTCACTGGGATCCCGCAAGGGGAGAC 300
QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
DB 301 TGTCTCTTGTGATCAGACGCGCAGATGCCAGATGAGTCAAGTACTTCTTTCGGGTG 360

QY 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPheLeuLysValThr 140
DB 361 GAGAGAGGAAGCTATGTGAGATATTAATTATGACATGGTCTTTCTTAAGATACAA 420
QY 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160
DB 421 GCCCTGACTCAGAAAGCCTGATGTCTATCATCCCGAGACCCCTGGAGCCGGGAGCGGTG 480
QY 161 ThrValIleCysValPheAsnTrpAlaPheGluGlyCysProProPheSerPheSerTrp 180
DB 481 ACGGTCACTGTGTGTTAACTGGCCCTTGAGAGAAATGTCACCCCTTCTTCTCTGG 540
QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
DB 541 ACGGGGGCTGCCCTCTCCCAAGAGAACCAACCAACCAAGCTTCCACTTCTCAGTCTC 600
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
DB 601 AGCTTCACGCCCAAGACCCAGAGACACGACACGACCTCACTGATGGACTTCTCC 660
QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
DB 661 AGAAAGGTTGTGACGACACAGAGACCCGTCCGACTCCGTGTGGCTATGGCCCCAGAGAC 720
QY 241 LeuValIleSerIleSerArgAspAsnThrProAspProProGluAsnLeuArgValMet 260
DB 721 CTGTGTATCAGCATTTTACGTGACACACACGCCAGATCTCTCAGAAACCTGAGAGTATG 780
QY 261 ValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuProVal 280
DB 781 GTTCCCAAGCAACACAGACAGAGCTCTGGAAACCTTGGAAACGACAGCTCTCCACGTA 840
QY 281 LeuGluGlyGlnSerLeuCysLeuValCysValThrHisSerProProAlaArgLeu 300
DB 841 CTGAGGAGCCAAACCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 301 SerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyValLeu 320
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QY 321 GluLeuProArgValAlaGlnValGlnHisGlnGlyLubPheCysHisAlaArgHisPro 340
DB 961 GAGGTGCTCGGTTCAGATGAGACACAGACCAAGAAAGTTCACCTCCAGCTCGGACACCA 1020
QY 341 LeuGlySerGlnHisValSerLeuSerLeuSerValHisTyrLysGlyLeuIleSer 360
DB 1021 CTGGGCTCCACGACAGCTCTCTCAGCCTCCGCTGCACATATAGAAAGGAGCATCTCA 1080
QY 361 ThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLysCys 380
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QY 381 LeuAlaLeuIleIleMetLysIleLeuProLysArgTrpThrGlnThrProArg 400
DB 1141 CTGGCCCTGATCATATGAAATTCATCCGAGAGACGAGATCTCAGACGAAACCCCAAG 1200
QY 401 ProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnValAlaProThrAlaGly 420
DB 1201 CCCAGGTTCTCCGGCAGACAGACATCTGTGATTAACATCAATGATGGTCCGACGGTGGC 1260
QY 421 ProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuPro 440
DB 1261 CCCCTGGTTCAGAAAGCGGAATCAAAACCCACCAACCACTCTCGGACCCCTTCTCA 1320
QY 441 ProGlyAlaProSerProGluSerLysAsnGlnLysGlnTyrGlnLeuProSer 460
DB 1321 CCAAGTGTCTCTCCCAAGATCAAAAGAGAACCAAGAAAGCACTATCACTTCCCACT 1380
QY 461 PheProGluProLysSerSerThrGlnAlaProGluSerGlnGluGluLeu 480
DB 1381 TTCCCAAGAACCAATATCATCTCACTCAAGCCCAAGATCCAGAGAGCCCAAGAGAGCTC 1440
QY 481 HisTyrAlaThrLeuAsnPheProGlyValAlaArgProArgProGluAlaArgMetProLys 500

Db 1078 TACACCTGCGAGGAGACAGGCTTGCTCCAGCAGCGAGCCCTGGACCTCTCTGTG 1137
 QY 253 -----ProProGluAsnLeuAlaArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
 Db 1138 CAGTATCTCTCCAGGAAACCTGAGAGTGTGTTCCCAAGCAAAACAGACAGTCTCTGGAA 1197
 QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysValCys 290
 Db 1198 AACCTGGAGACGGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCCTTGCTGCTCTGT 1257
 QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
 Db 1258 GTCACACACAGACACCCCGCAGCAGCTGAGTGCAGCCAGAGGGGAGAGTCTGAGC 1317
 QY 311 ProSerGlnProSerAspProGlyValLeuGluLeuProAlaArgValGlnValGluSer 330
 Db 1318 CCCTCCAGCCCTGAGACCCCGGGGCTCTGAGCTGCTCGGTTCAAGTGAACACGAA 1377
 QY 331 GlyLeuPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
 Db 1378 GGAGAGTTACACTGCGACGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCTGAGCTC 1437
 QY 351 SerValHisTyr----- 354
 Db 1438 TCCGTGACTACTCCCGAAGCTGTGGGCCCTCTGCTCTGAGAGGCTGAGGGTCTG 1497
 QY 354 ----- 354
 Db 1498 CACTGCAGCTGCTCTCCAGCAGCCGCCGCCCTCTGCGCTGGTGGCTTGGGGAG 1557
 QY 354 ----- 354
 Db 1558 GAGTGTCTGGAGGGGAAACAGACAGCCAGACTCTTCGAGGTCACCCCGACGCTACGCCGG 1617
 QY 354 ----- 354
 Db 1618 CCCTGGGGCCAAACGCTCCCTGAGCTCCATGAGAGGCTCAGCTCCGCCCTCAGGCTCCGC 1677
 QY 355 -----Lys 355
 Db 1678 TGTGAGGCTGGAACGTCCATGGGGCCCGAGTGCATCCCTGCAGCTCCCGAATTAAG 1737
 QY 356 LysGlyLeuLeuSerThrAlaPheSerAsnGlyValaPheLeuGlyIleGlyIleThrAla 375
 Db 1738 AAGGAGCTCATCTCAAGGCAATCTCCACAGGAGCGCTTCTGGAAATCGGATCAGCGCT 1797
 QY 376 LeuLeuPheLeuCysLeuAlaLeuIleLeuMetLysIleLeuProLysArgArgThrGln 395
 Db 1798 CTCTTTCTCTGCTGCTGCGCTGATCATGATGAAGATCTACCGAAGAGACGAGCTCAG 1857
 QY 396 ThrGluThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnVal 415
 Db 1858 ACAGAAACCCGAGGCGCCAGGTTCTCCGCGACAGCGATCCGGAATTCATCAATCAAGTG 1917
 QY 416 ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro 435
 Db 1918 GTCCCGAGGCTGGCCCTGGCTCAGAACCGGATTCAGAAAGCCACCAACAGAGTCTCT 1977
 QY 436 ArgThrProLeuProProGlyValaProSerProGluSerLysLysAsnGlnLysGln 455
 Db 1978 CGAGACCCCTTCTCAGCAGGTGCTCCCTCCCGAATCAAAAGAAAGAACCGAAGAACAG 2037
 QY 456 TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGlnGlu 475
 Db 2038 TATCAGTTGCCAGTTCCAGAACCAATCATTCACCTAAGCCCGAGATCCAGGAG 2097
 QY 476 SerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyValaArgProArgProGlu 495
 Db 2098 AGCCAGAGGAGCTCATTTATGCCAGCTCAACTCCAGGCGCTCAGAGACCCAGGCGTGGAG 2157
 QY 496 AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512
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Db 2158 GCCCGATGCCCAAGGCGACCCAGCGGATTTATGCAAGTCAAGTCCAA 2208
 RESULT 3
 ABK43373
 ID ABK43373 standard; cDNA: 3024 BP.
 XX
 AC ABK43373;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2.
 XX
 KW Human: sialic acid-binding Ig-related lectin; Siglec; asthma;
 KW immune system disease; leukaemia; allergy; inflammatory disease;
 KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
 KW psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200208257-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 20-JUL-2001; 2001WO-US23082.
 XX
 PR 21-JUL-2000; 2000US-220139P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Longphre M, Chang H, Whitney G;
 DR WPI: 2002-241565/29.
 DR P-PSDB: AAU87087.
 XX
 PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
 PT molecules useful for treating immune system diseases such as asthma,
 PT leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
 PT
 XX
 PS Example 11; Figure 6; 20pp; English.
 XX
 CC The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
 CC related lectin) protein (I). Pharmaceutical compositions comprising (I)
 CC are useful for treating immune system diseases such as asthma, leukaemia
 CC or other allergic or inflammatory diseases. Extracellular domains of (I)
 CC represent potential markers for screening, diagnosis, prognosis,
 CC follow-up assays, and imaging methods. (I) is useful as a target for
 CC drugs which inhibit inflammation, tissue damage and remodeling in
 CC asthma, and inflammatory diseases such as allergic rhinitis,
 CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
 CC conjunctivitis, etc. (I) is also useful for monitoring the course of
 CC disease or disorders, and for identifying agents that bind with and/or
 CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
 CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
 CC methods, and to detect the presence and/or amount of SIGLEC-BMS
 CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
 CC (II) are useful as nucleic acid probes are useful for screening genomic
 CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
 CC number is determined for detecting diseases or disorders associated with
 CC SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
 CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
 CC and in diagnostic imaging technology. ABK43360-ABK43411 represent
 CC human SIGLEC coding sequences and PCR primers of the invention.
 XX
 SQ Sequence 3024 BP; 699 A; 933 C; 790 G; 602 T; 0 other;
 Alignment Scores:
 Pred. No.: 5,94e-176 length: 3024
 Score: 2580.50 Matches: 510
 Percent Similarity: 73.31% Conservative: 1
 Best Local Similarity: 73.17% Mismatches: 1
 Query Match: 95.36% Indels: 185

DB:		24	Gaps :	2
US-09-937-636-3 (1-512) x ABRK43373 (1-3024)				
OY	MetleuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg	20		
Db	ATGGTACTGCACAGCTGCTGTCTCCGTGGCGGGGTCCCAAGCATGGAAGGGAGA	188		
OY	PheThrPilearValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro	40		
Db	TTCGTGATACAGAGTGCAAGANTCAGTAGTGGTGGCGAAGGCCCTGTGATCTCTGTGCC	248		
OY	CysSerPheSerTyrrProArgGlnAspTrpThrGlySerThrProAlaTyrgLyrrTrp	60		
Db	TGCTCTTTCTCTCTACCCTCCGACAAGACAGCACAGAGGTCTACCCAGCTTATGGCTACTGG	308		
OY	PheValAlaValThrGluThrThrThyLysGlyAlaProValAlaThrAsnHisGlnSerArg	80		
Db	TTCAAAGCAGAGCATGAGAACCAACAAAGGCTCTCTGTGGCCAAACACACAGTCGA	368		
OY	GluValGluMetSerThrArgGlyValArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	100		
Db	GAGGTGCMAATGACAGCACCCGGGGCCGATTCCAAGCTCACTGGGAGATCCCGCAAGGGGNA	428		
OY	CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrrPhePheArgVal	120		
Db	TGCTCTTGGTGATCAGAGACGGCCAGATGCAGAGTGAATGATCAAGTAATCTTTTCGGGTG	488		
OY	GluArgGlySerTyrrValArgTyrrAsnPhenMetAsnAspGlyPhePheLeuLysValThr	140		
Db	GAGAGAGAACCTATGTGACATATAATTCAATGAAACGATGGCTTTCTTAAAAGTAAACA	548		
OY	AlaLeuThrGlnLysProAspValTyrrIleProGluThrLeuGluProGlyGlnProVal	160		
Db	GCCCTGACTCAGAAAGCTGATGTCTACTATCCCCAGAACCTCTGGAGACCCGGGACGGGTG	608		
OY	ThrValIleCysValPheAsnTrpAlaPheGluLucysProProProSerPheSerTrp	180		
Db	ACGGTCACTGTGTGTTTTAACTGGAGCCCTTGTAGGAATGCCACCCCCTTTCTTCCTGG	668		
OY	ThrGlyAlaAlaLeuSerSerGlnGlyThrIrysProThrTrpSerHisPheSerValLeu	200		
Db	ACGGGGGCTGCCCTCTCTCCCAAGAAACCAACCAAGACCTCCCACTTTCAGTGTCTC	728		
OY	SerPheThrProArgProGlnAspHisAspPheArgPheLeuTrpCysHisValAspPheSer	220		
Db	AGCTTCACGCCCAACCCCAAGACACACAAACCCGACTCACTGCTCATGTGACTTCTCC	788		
OY	ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrrAlaProArgAsp	240		
Db	AGAAAGGCTGTGAGGGCAGACAGAGGCGGTCCGACTCGTGTGGCTATGGCCCCAGAAAC	848		
OY	LeuValIleSerIleSerArgAspAsnThrProasp-----	252		
Db	CTTGTTATACACATTTCACGTGACAAACACGCCACCCCTYGAGCCCAACCCAGGAAT	908		
OY	-----	252		
Db	GTCCCATACCTGGAGAGCCCAAAAAAGGCCAGTTCTCGGGCTCTCTGTGCTGACAGC	968		
OY	-----	252		
Db	CAGCCCTCTGCACACTGAGCTGGGTCTCGAAGAACAGATCTCTCTCTGCCATCC	1028		
OY	-----	252		
Db	TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCGGGGTGAAGGCTGGGGAATTCAAGGGCC	1088		
OY	-----	252		
Db	TACACACTCCGAGGAGAACAGAGCTTGGTGCTCCACAGCAGCAAGCCCTTGACCTCTCTGTG	1148		
OY	-----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	270		

Db	1149	CAGTATCTCCAGAGAACCTGAGATGATGGTTTCCCAACCAACAGAGACAGCTCTGAA	1208
OY	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyInsLeuCysLeuValCys	290
Db	1209	AACCTTGGGAAGCAGCTCTCTCTCCAGTACTGAGGGGCCAAAGCCTGTGCTGTCTGT	1268
OY	291	ValThrHisSerSerProProAlaArgLeuSerThrGlnArgGlyGlnValLeuSer	310
Db	1269	GTCAACACAGACAGCCCCAGCCAGAGCTGAGTGGAGCCAGAGGGAGGATCTGAGC	1328
OY	311	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu	330
Db	1329	CCCTCCAGAGCCTCAGACCCCGGGGGCTCTGGAGCTGCTGGGTTCAAGTGGAGCACGAA	1388
OY	331	GlyValuPhePhePheCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1389	GGAGAGTTTCACCTTCCACAGCTCGGACCCACCTGGGGTCCAGACAGTCTCTCAGGCTC	1448
OY	351	SerValHisTyr-----	354
Db	1449	TCCGTGCACACTACTCCCGGAAGCTCTGGGCCCTCTCTGCTCTGTGGAGGCTGAGGGTCTG	1508
OY	354	-----	354
Db	1509	CACTCAGACGTCCTCTCCAGAGCCAGCCGAGCCCTCTCTGCGCTGTGGCTTGGGAG	1568
OY	354	-----	354
Db	1569	GAGCTGCTGGAGGGGAACAGCAGCCAGGACTCTTCGAGGTCAACCCCAAGCTCAGCGGG	1628
OY	354	-----	354
Db	1629	CCCTGGGGCAACACTCTCCCTGAGGCTCCATGGAGGCTCAGCTCCGGCTCAGGCTCCGC	1688
OY	355	-----Lys	355
Db	1689	TGTGAGGCGCTGGAAAGTCATGAGGGGCCAGAGTGGATTCATCTCGAGCTGCCAGATAAG	1748
OY	356	LyseGlyLeuLeuSerThrAlaPheSerAsnGlyLalaPheLeuGlyIleGlyIleThrAla	375
Db	1749	AAGGAGCTCATCTTAAGGCAATTCCTCCACCGAGCGTTCTGGGAATCGGATCAGCGCT	1808
OY	376	LeuLeuPheLeuCysLeuAlaLeuIleIleMetCysIleLeuProLysArgArgThrGln	395
Db	1809	CTTCTTTTCCCTGCTGCGCCCTGATCATCATGAAGATTCTACCGAAGAGCGACTCAG	1868
OY	396	ThrIuThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnVal	415
Db	1869	ACAGAAACCCCGAGGGCCAGGTTCTCCCGCAGACAGCATCTCGATTACATCAATGTG	1928
OY	416	ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro	435
Db	1929	GTCGCCGAGCGGTGGCCCCCTGGCTCAGAAAGGGATAGAAAGGCCACACCAACAGTCTT	1988
OY	436	ArgThrProLeuProProGlyAlaProSerProLeuSerLysAsnGlnLysGln	455
Db	1989	CGAGACCCCTCTCCACACGAGTGCCTCCCTCCCAATCAAGAAAGAACACGAAAAACAG	2048
OY	456	TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGlnGlu	475
Db	2049	TATCAGTTGCCCACTTCCAGAACCCAAATCATCACTCAAGCCCAAGATCCACAGAG	2108
OY	476	SerGlnGluGluLeuHisIleTyrAlaThrLeuAsnPheProGlyValAlaArgProArgProGlu	495
Db	2109	AGCCCAAGAGGAGCTCCATTATGCCAGCTCAACTTCCAGGCGTCAGACCCAGGCGCTGAG	2168
OY	496	AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln	512
Db	2169	GCCCGGATGCCCAAGGCGACCCAGCGGATTTATGCAGAGTCAAGTTCCAA	2219

RESULT 4
ABK43360

ID ABK43360 standard; cDNA; 2565 BP.
 AC ABK43360;
 DT 05-JUN-2002 (first entry)
 DE DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-V3a.
 XX
 XX Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
 KW immune system disease; leukaemia; allergy; inflammatory disease;
 KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
 KW psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.
 XX
 OS Homo sapiens.
 PN WO200208257-A2.
 PD 31-JAN-2002.
 XX
 XX 20-JUL-2001; 2001WO-US23082.
 PF
 XX 21-JUL-2000; 2000US-220139P.
 PR
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Longphre M, Chang H, Whitney G;
 PI
 XX WPI: 2002-241565/29.
 DR
 XX P-PSDB; AAU87074.
 XX
 PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
 PT molecules useful for treating immune system diseases such as asthma,
 PT leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
 PT
 PS Claim 11; Figure 2A; 209pp; English.
 XX
 XX The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
 CC related lectin) protein (I). Pharmaceutical compositions comprising (I)
 CC are useful for treating immune system diseases such as asthma, leukaemia
 CC or other allergic or inflammatory diseases. Extracellular domains of (I)
 CC represent potential markers for screening, diagnosis, prognosis,
 CC follow-up assays, and imaging methods. (I) is useful as a target for
 CC drugs which inhibit inflammation, tissue damage and remodeling in
 CC asthma, and inflammatory diseases such as allergic rhinitis,
 CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis,
 CC conjunctivitis, etc. (I) is also useful for monitoring the course of
 CC disease or disorders, and for identifying agents that bind with and/or
 CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid
 CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
 CC methods, and to detect the presence and/or amount of SIGLEC-BMS
 CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.
 CC (II) are useful as nucleic acid probes are useful for screening genomic
 CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy
 CC number is determined for detecting diseases or disorders associated with
 CC SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also
 CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins
 CC and in diagnostic imaging technology. ABK43360-ABK43411 represent
 CC human SIGLEC coding sequences and PCR primers of the invention.
 CC
 XX
 XX
 SQ Sequence 2565 BP; 627 A; 765 C; 656 G; 517 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 2 7e-154 Length: 2565
 Score: 2278.00 Matches: 452
 Percent Similarity: 75.25% Conservative: 1
 Best Local Similarity: 75.08% Mismatches: 1
 Query Match: 84.18% Indels: 148
 DB: 24 Gaps: 2
 US-09-937-636-3 (1-512) x ABK43360 (1-2565)
 1 MetLeuLeuProLeuLeuLeuSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20

Dd			129	ATGCTACGCCA	CAGTCTGTCTGCTCCTGGCTCTGGCGGCTCCCAAGCTTGATGGAGA	188
Oy	21	Phe	rPrIle	aArgVal	GIngluSerValMetValProGluGlyLeuCysIleSerValPro	40
Dd	189	TTC	GCATAC	CGAGTGCAGAGTCACTGATGGTCCGGAAGGCGCTGTCATCTGTGGCCC	248	
Oy	41	Cys	SerPhe	SetrTy	rProArgInsprThrPhgIyserThrProAlaTrcGlyTryp	60
Dd	249	TGCTTTCT	CTCTACC	CCCCGACAAGACTGGACAGGGTCTACCCCACTTATGGCTTA	308	
Oy	61	Phe	tylAla	ValThrGlutThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	80	
Dd	309	TTCAAAGCA	AGTAGT	GAGAACCAACAAAGGGTGTCTCTGGCCCAAAACCAACAGATGCA	368	
Oy	81	GI	ValAla	GluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	100	
Dd	369	GAGGGGAAA	TAGAGCAC	CGGGGGCGATTCCAGCTCATCGGGGATCCCGCCAAAGGGGAAC	428	
Oy	101	Cys	SerLeu	ValIleArgAspAlaGlnMetGlnAspGluSerGlnTrpPhePheArgVal	120	
Dd	429	TGCTCCTTG	TCATCAT	GAGAGACCGCGAGATGCAGAGATGATCAAGATCTTCTTGGGTG	488	
Oy	121	GI	uarGly	SetrTyValArgTryAsnPheMetAsnAspGlyPhePheLeuLysValItr	140	
Dd	489	GAGAGAGAA	AGGTATG	TGATGATATATTCATGAACAGATGGGTCTCTTTATAAAGTAACA	548	
Oy	141	Ala	LeuThrGlnLys	ProaspValnyrIleProGluThrLeuGluProGlyGlnProval	160	
Dd	548	-----				548
Oy	161	Thr	ValIle	CysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp	180	
Dd	548	-----				548
Oy	181	Thr	GlyAlaAla	LeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValleu	200	
Dd	549	-----				549
Oy	201	Ser	PheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	220		
Dd	555	AGCTTCAC	GGCCAGAC	CCCCAGAGACCAACACCGACTCACCCTGCATGTGGACTTCTCC	614	
Oy	221	Arg	LysGly	ValIleSerAlaGlnArgThrValArgLeuArgValAlaArgAlaProArgAsp	240	
Dd	615	AGAAAGGG	GTGTAGG	CGACAGAGGACCTGTCACCTGTTGGCTATGCCCCACAAGAC	674	
Oy	241	Leu	ValIle	SerIleSerArgAspAsnThrProAsp	252	
Dd	675	CTTGTTAT	CAGATTTC	ACAGTGCACAACAGCCAGCCCTGGAAGCCCCAGCGGGAAT	734	
Oy	252	-----				252
Dd	735	GTCCCAT	ACTCTGGA	AGCCCAAAAGCGCAGTTCCTCGGCTCTCTGTGCTGTGACAGC	794	
Oy	252	-----				252
Dd	795	CAGCCCC	CTGCCAC	ACTGAGCTGGGTCTGCAAGAACAGAGTCTCTCTCTGTCCTCCATCCC	854	
Oy	252	-----				252
Dd	855	TGGGGCC	CTTAGAC	CCCTGGGGCTGCAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC	914	
Oy	252	-----				252
Dd	915	TACACCT	GCGGAG	CGGAGAACAGGCTTGCTCCACAGCAGAGCCCTGCACCTCTCTGTG	974	
Oy	253	-----				253
Dd	975	CAGTATTC	CTCCAG	AACCTGAGAGTATGATGTTCCCAAGCAAAACAGGACAGCTCTGGAA	1030	
Oy	271	Asn	LeuGlyAsn	GlyThrSerLeuProValLeuGluGlyGlnSerLeuGlySleuValCys	290	

Db 1035 AACCTGGAGACGGACGCTCTCTCCAGTACTGGAGGCCAAAGCCTGCTGTCTGT 1094
QY 291 VAlThrHIsSerSerProProAlaArGleuSerTIPThGlnArGlyGlnValleuSer 310
Db 1095 GTCAACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGAGAGGTTCTGACG 1154
QY 311 ProSerGlnProSerAspProGlyValleuGlnleuProArGValGlnValGlnHISgln 330
Db 1155 CCCTCCAGCCTTCAGAGACCCGGGGGCTCGAGAGTCCCTCGGGTTCAATGGAGCGACGA 1214
QY 331 GlyGluPheThrCysHISAlaArGHisPLeuGlySerGlnHISValSerleuSerLeu 350
Db 1215 GGAGAGTTCTACCTGGCACCGCTCGGACCCACTGGGGTCCACACACTCTCTCTCAAGCTTC 1274
QY 351 SerValHISrTyLysGlySerGlyleuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
Db 1275 TCCGTCGACTATAGAGAGGACTCATCTTAAGGCAATTTCCACAGGAGCGTTCTGGGA 1334
QY 371 IlegIyIleThrAlaLeuIleuPheLeuCysleuAlaLeuIleIleuTySileuPro 390
Db 1335 ATCGGCATCAGCGCTCTTCTTTCTCTCTGCTGCGCCCTGATCATGTAAGATTCTACCG 1394
QY 391 LysArGArGThrGlnThrGlnuThrProArGProArGPhSerArGHisSerThrIleu 410
Db 1395 AAGACAGCGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGCACAGCAGATCTTG 1454
QY 411 AsPTyTlLeAsnValAlaProThrAlaGlyProLeuAlaGlnLysArGAsnGlnLysAla 430
Db 1455 GATTACATCATGTGTGTCGACGGCTGGCCCCCTGGCTCAGAGCGGATCAGAAAGGCC 1514
QY 431 ThrProAsnSerProArGThrProleuProProGlyAlaProSerProGlySerLysLys 450
Db 1515 ACACCAAGACGTCCTCGACCCCTCTTCCACAGGAGTCCCTCCCAATCAAGAAGAG 1574
QY 451 AsnGlnLysLysGlnTyGlnleuProSerPheProGlnProLysSerSerThrGlnAla 470
Db 1575 AACCGAAAGAACAGATCATGTTGCCCATTTCCAGAACCCAAATCATCCACTCAAGCC 1634
QY 471 ProGlnSerGlnGlnSerGlnGlnleuIleuHISrTyTAlaThrLeuAsnPheProGlyVal 490
Db 1635 CCAGAAATCCAGAGAGCCAAAGAGAGCTCCATATGCCAGCTCACTTCCAGGCGTTC 1694
QY 491 ArGProArGProGlnAlaArGmetProLysGlyThrGlnAlaAsPTyTAlaGlnValLys 510
Db 1695 AAGACCCAGGCTGAGAGCCCGGATGCCCAAGGCGACCCAGCGGATATCAGAAAGTCAAG 1754
QY 511 PheGln 512
Db 1755 TTCCAA 1760

RESULT 5
AAZ34109
ID AAZ34109 standard; cDNA: 2764 BP.
XX
AC AAZ34109;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO940 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.

PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082569.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.

Db	1252	ATCGGCATCAACGGCTCTTCTTTCCTCTGCTGGCCCTGATCATCATGAAATTCCTACCG	1311		
Qy	391	LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu	410		
Db	1312	AAGAGACGAGACTCAGACAGAAACCCGAGGCCAGGTTCTCCGGCACAGCAGTCCTG	1371		
Qy	411	AspArgTrlLeuValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla	430		
Db	1372	GATTACTCATCATGTGGTCCGACAGCGCTGGCCCTGGCTCAGAAAGCGGAATCAGAAAGCC	1431		
Qy	431	ThrProAsnSerProArgThrProLeuProGlyAlaProSerProGluSerLysLys	450		
Db	1432	ACACCAAAACAGCTCTCGGACCCCTCCCTCCACAGAGTGTCTCTCCCAAGATCAAAAGAG	1491		
Qy	451	AsnGlnLysLysGlnTyrglnLeuProSerPheProGluProLysSerSerThrGlnAla	470		
Db	1492	AACCAAGAAAAAGCAGTATCAGTTGCCAGATTCCAGAACCAATCATCCATCAAGACC	1551		
Qy	471	ProGluSerGlnGluSerGlnGluLeuHisTyrAlaThrLeuAsnPheProGlyAla	490		
Db	1552	CCAAATATCCCAAGAGACCAAGAGAGACTCCATTATGCCAGCTCAACTTCCAGGCGCTC	1611		
Qy	491	ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys	510		
Db	1612	AGACCCAGGCGCTGAGGCCGATGCCAGATGCCAAGGGACACCAAGCGGATTATGCAGAACTCAAG	1671		
Qy	511	PheGln 512			
Db	1672	TTCCAA 1677			
RESULT 6					
AAC78510	AAC78510 standard; cDNA: 2764 BP.				
XX	AAC78510;				
XX	08-FEB-2001	(first entry)			
DE	Human PRO940 (UNQ477) nucleotide sequence SEQ ID NO:258.				
KM	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;				
XX	expressed sequence tag; detection; cancer; ss.				
OS	Homo sapiens.				
PN	WO200053756-A2.				
PD	14-SEP-2000.				
PF	18-FEB-2000; 2000MO-US04341.				
XX	08-MAR-1999;	99MO-US05028.			
PR	12-MAR-1999;	99US-0123957.			
PR	29-MAR-1999;	99US-0126773.			
PR	21-APR-1999;	99US-0130232.			
PR	28-APR-1999;	99US-0131445.			
PR	14-MAY-1999;	99US-0134287.			
PR	23-JUN-1999;	99US-0141037.			
PR	26-JUL-1999;	99US-0145698.			
PR	29-OCT-1999;	99US-0162506.			
PR	30-NOV-1999;	99MO-US28313.			
PR	02-DEC-1999;	99MO-US28551.			
PR	16-DEC-1999;	99MO-US28565.			
PR	30-DEC-1999;	99MO-US30095.			
PR	16-DEC-1999;	99MO-US31243.			
PR	30-DEC-1999;	99MO-US31274.			
PR	05-JAN-2000;	2000MO-US00219.			
PR	06-JAN-2000;	2000MO-US00277.			
PR	06-JAN-2000;	2000MO-US00376.			
XX	(GETH) GENENTECH INC.				
XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;				

PI	Betrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AJ, Hillan KJ, Kljavan IJ, Kuo SS, Napier MA, Pan J, Peoni NR, Roy MA, Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI, WPI: 2000-611443/58.		
DR	P-PSDB: AAB4280.		
XX			
PT	Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -		
XX			
PS	Claim 2; Fig 92: 636pp; English.		
XX			
CC	AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytosolic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.		
CC			
XX			
XX	Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 other:		
XX			
SD			
Alignment Scores:			
Pred. No.:	2,54e-153	Length:	2764
Score:	2265.00	Matches:	450
Percent Similarity:	74.92%	Conservative:	1
Best Local Similarity:	74.75%	Mismatches:	3
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KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX Homo sapiens.
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XX 20-SEP-2001.
XX 28-FEB-2001; 2001WO-US06520.
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AC ABX98211;
DT 19-MAY-2003 (first entry)
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KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cytosolic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW cartilage disorder; sports injury.
XX
OS Homo sapiens.
XX
PN US2003036156-A1.
PD 20-FEB-2003.
XX
PE 02-JUL-2002; 2002US-0188767.
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Alignment Scores:
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Score: 2265.00
Percent Similarity: 74.92%
Best Local Similarity: 74.75%
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Gaps: 2

US-09-937-636-3 (1-512) x ABX98211 (1-2764)

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DB 46 ATGCTACTGCACACGCTGCTGCTCCCTGCGGCGGTCGCCAGGCTATGATGGAGAGA 105
QY 21 PheTrpIleArGyValGlnGlnSerValMetValProGluLcylLeuCysIleSerValPro 40
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Qy      391 LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu 410
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Qy      411 AspTyrIleAsnValIleProThrAlaGlyProLeuAlaGlnLysArgAsnGlnValAla 430
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Qy      431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys 450
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Qy      491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510
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Db      1672 TTCCAA 1677

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AC ABX98713;
AC 20-MAY-2003 (first entry)
DE Novel human secreted and transmembrane protein PRO940 cDNA.
XX Human; secreted protein; transmembrane protein; cytosolic;
XX gene therapy; TNF-Agonist-Alpha; Chondrocyte stimulator; tumour;
XX adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour;
XX gene; ss.
OS Homo sapiens.
XX
XX US2003036157-A1.
XX
XX 20-FEB-2003.
XX
XX 02-JUL-2002; 2002US-0188769.
XX
XX 16-SEP-1998; 98WO-US19330.
XX
XX 07-OCT-1998; 98WO-US21141.
XX
XX 01-DEC-1998; 98WO-US25108.
XX
XX 08-MAR-1999; 99WO-US05028.

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 Db 1672 TTCCA 1677
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 AC ACA05758;
 DT 29-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein (PRO) cDNA #59.
 XX
 KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2003036162-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 12-JUL-2002; 2002US-0194423.
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 PR 28-JUL-2000; 2000WO-US20710.
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 PR 20-DEC-2000; 2000WO-US34956.
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 PR 07-OCT-1998; 98US-0168978.
 PR 06-NOV-1998; 98US-0187368.
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 PR 16-AUG-2001; 2001US-0931836.
 PR 28-AUG-2001; 2001US-0941992.
 PR 04-SEP-2001; 2001US-0946374.
 PR 15-JAN-2002; 2002US-0052586.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2003-332039/31.
 DR P-PSDB; AB067464.
 XX
 XX New secreted and transmembrane PRO polypeptides and nucleic acids,
 PT useful in gene therapy. In chromosome and gene mapping, as chromosome
 PT markers, in tissue typing, and in chromosome identification
 XX
 PS Claim 2; Fig 117; 706pp: English.
 XX
 CC The invention discloses human nucleic acids encoding secreted and
 CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
 CC specifically binds to the PRO polypeptide, a method for stimulating the
 CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
 CC contacting the blood a PRO polypeptide, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells by contacting the
 CC cells with a PRO polypeptide, a method for detecting the presence of a
 CC tumour in a mammal and an oligonucleotide probe derived from any of the
 CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
 CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
 CC preparing PRO polypeptides by recombinant techniques and in gene therapy
 CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
 CC as molecular weight markers for protein electrophoresis purposes, for
 CC chromosome identification, as chromosome markers, as therapeutic agents,
 CC for stimulating the release of TNF-alpha from human blood, for
 CC stimulating the proliferation or differentiation of chondrocytes and
 CC detecting the presence of a tumour. The PRO polypeptides and nucleic
 CC acids may also be used diagnostically for tissue typing. The sequences
 CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
 CC polypeptides of the invention.
 XX
 SO Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 other;

Alignment Scores: 2.54e-153 Length: 2764
 Pred. No.: 2265.00 Matches: 450
 Score: 74.92% Conservative: 1
 Percent Similarity:

Best Local Similarity:	74.75%	Mismatches:	3
Query Match:	83.70%	Indels:	148
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QY	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	166 TGTCTTCTTCTCTACCCCGGACAAACACTGACAGGGTCTACCCCACTTATGGCTACTGG	225
QY	61 PheIysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	80
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QY	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuGlyValCys	290
Db	952	AACCTGGGAACGGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGGCTGGTCTGT	101
QY	291	ValThrHisSerSerProProAlaArgLeuSerTTPThrGlnArgGlyGlnValLeuSer	310
Db	1012	GTCACACACACACAGCCGCCACCCAGCGGTGAGCTGGACCTGACCAAGGGGACAGGTTCTGACC	107
QY	311	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnHisGlu	330
Db	1072	CCCTCCCGCCCTCGAGACCCCGGGGTCTCTGGAGCTGCTCCGGGTTCAAGTGAACGACGA	113
QY	331	GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1132	GGAGAGTTACACCTGGCAGCTGTGGCACCCACTGGGCTCCACACAGCTCTCTCAGCCCTC	119
QY	351	SerValHisTyrLysLysGlyLeuLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly	370
Db	1192	TCCGTGCCTATTAAGAAAGGAGCTCATCTCAACGGGATCTCCAAAGGAGACGTTTCTGGGA	125
QY	371	IleGlyIleThrAlaLeuLeuPheLeuGlySerLeuAlaLeuIleIleMetLysTlleLeuPro	390
Db	1252	ATCGGCATACAGGCTCTTCTTTCTCTGTGCTGGCCCTGATCATATGATGAAGTTCTACCG	131
QY	391	LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu	410
Db	1312	AAGAGACGAGCTCAGACAGAAACCCGAGGCCAGAGTTCTCCGGCAGACAGCATCTCTG	137
QY	411	AspTyrIleAsnValValProThrAlaGlyProIleAlaGlnLysArgAsnGlnLysAla	430
Db	1372	GATTACATCAATGTGCTCCGACGGCTGGCCCCCTGGCTCAAGACGGAAATGAGAAAGCC	143
QY	431	ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys	450
Db	1432	ACACCAAAACAGTCTCGGACCCCTCTCCACAGAGTGTCCTCCCAAGATCAAAAGAG	149
QY	451	AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla	470
Db	1492	AACCAAGAAAAAGCAGTATCACTGGCCAGTTGCCAGAAACCAAAATCAATCCACTCAAGCC	155
QY	471	ProGluSerGlnGlnSerGlnGlnLeuHisTyrAlaThrLeuAsnPheProGlyVal	490
Db	1552	CCAGATCCCGAGGAGGCCAAGAGAGCTCCATTATGCCACGCTCAACTTCCAGAGCGCTC	161
QY	491	ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys	510
Db	1612	AGACCACAGGCGTGAAGGCCGGATGCCAAAGGCCACACGAGCGGATATTCACAAGTCAAG	167
QY	511	PheGln 512	
Db	1672	TTCCAA 1677	
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ABX92481			
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XX	ABX92481;		
XX	08-MAY-2003	(first entry)	
DE	cDNA encoding human PRO940 polypeptide.		
KW	Human: PRO polypeptide; secreted and transmembrane protein;		
KW	immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;		
KW	cardiac insufficiency; nervous system disorder; kidney disorder;		
KW	bone disorder; cartilage disorder; arthritis; tumour; wound healing;		
KW	genetic disorder; cytostatic; antidiabetic; antiinflammatory;		
KW	antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;		


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KM cardiant; gene; ss.
XX Homo sapiens.
XX US2002169284-A1.
XX
XX 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-0978697.
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XX 07-OCT-1998; 98WO-US21141.
XX 20-NOV-1998; 98WO-US24855.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99WO-US05190.
XX 14-MAY-1999; 99WO-US10733.
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XX 30-DEC-1999; 99WO-US31243.
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XX 02-MAR-2000; 2000WO-US05841.
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XX 17-OCT-1997; 97US-062250P.
XX 03-NOV-1997; 97US-064249P.
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XX 21-NOV-1997; 97US-066364P.
XX 10-MAR-1998; 98US-077450P.
XX 11-MAR-1998; 98US-077632P.
XX 11-MAR-1998; 98US-077641P.
XX 11-MAR-1998; 98US-077649P.
XX 12-MAR-1998; 98US-077791P.
XX 13-MAR-1998; 98US-078004P.
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XX 20-MAR-1998; 98US-078910P.
XX 20-MAR-1998; 98US-078936P.
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XX 25-MAR-1998; 98US-079656P.
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XX 27-MAR-1998; 98US-079664P.
XX 27-MAR-1998; 98US-079689P.
XX 27-MAR-1998; 98US-079728P.
XX 27-MAR-1998; 98US-079786P.
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XX 30-MAR-1998; 98US-079923P.
XX 26-MAY-1981; 81US-0267213.
XX 17-MAR-1998; 98US-0040220.

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PR 26-JUN-1998; 98US-0105413.
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PR 06-NOV-1998; 98US-0187368.
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PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
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PR 14-MAY-1999; 99US-0380137.
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PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709228.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
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PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
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PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
XX Ferrara N, Filvarioff E, Fong S, Gao W, Gerber H, Gritlsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ;
XX Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-288163/28.
XX
XX P-PSDB; AB061110.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating cancer, kidney diseases, bone,
XX cartilage disorders and immune deficiencies
XX
XX Claim 2; Fig 92; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX PRO polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for
XX linking bioactive molecules to cells expressing PRO polypeptides,
XX for modulating biological activities of cells expressing PRO
XX polypeptides, and for identifying agonists or antagonists. The
XX bioactive molecule maybe a toxin, radiolabel or antibody, and causes
XX apoptosis or death of the cell. The PRO polypeptides are useful for
XX treating immune disorders, diabetes or hyper- or hypo-insulinemia,
XX cardiac insufficiency, nervous system disorders, kidney disorders,
XX bone and cartilage disorders or arthritis, tumours, and wound healing.
XX The polynucleotide sequences encoding PRO polypeptides are useful as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, in the preparation of PRO polypeptides, for
XX generating transgenic animals or knockout animals, for the genetic
XX analysis of individuals with genetic disorders, and in gene therapy.
XX The present sequence encodes a human PRO polypeptide of the invention.
XX Note: The sequence data for this patent was obtained in electronic
XX format directly from the USPTO web site at
XX seqdata.uspto.gov/psipdIdentify.html.
XX
XX Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2.54e-153 Length: 2764
XX Score: 2265.00 Matches: 450
XX Percent Similarity: 74.928 Conservative: 1
XX Best Local Similarity: 74.758 Mismatches: 3
XX Query Match: 83.708 Indels: 148

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OY	21 PheTPILeArgValGInGInLysSerValMetValProGluGlyLeucySTIleSerValPro	40		
Dd				
OY	41 CysSerPheSerTYrProArgGlnAsnPTripThGlySerThrProLaTYrGlyTYrTrp	60		
Dd	166 TCGCTTTCTTCCTACCCCCGACAAGACTGGACAGGGTCTAACCCACTTAGGCTACTGG	225		
OY	61 PheLYsAlaValIThrGluThrThrylsglyAlaProValAlaThrAsnHISgInSerArg	80		
Dd	226 TTCAAAAGCAGTGACTGAGACAACCAGGGGTGCTCTGTGGCCCAAACCCAGAGTCGA	285		
OY	81 GluValGInMetSerThrArgGlyArgPheGInLeuThrglyAspProAlaLYsGlyAsn	100		
Dd	286 GAGGTGGAAATAGCACCCCGGGGCCATTTCACCTACTGGGATCCCGCCAAGGGGAC	345		
OY	101 CysSerLeuValILEarGAspAlaGInMetGInAspGLusergIntYrPhePheArgVal	120		
Dd	346 TCCTCTCTTGATCATCAGACACGCGAGATGCAAGAGAGACACAGTAACCTCTTTCGGGTG	405		
OY	121 GluArGlySerTYrValArgTyraSnPheMetAsnAspGlyPhePheLeuLYsValThr	140		
Dd	406 GAGAGGAGAGCTAATGTGACATATAATTTACATGACAGATGGGTTCTTTCAAAAGTACA	465		
OY	141 AlaLeuThrgInLysProAspValTYrILEproGluThrLeuGluProGlyInProval	160		
Dd	465 -----	465		
OY	161 ThrValILEcyValPheAsnTriPalapheGluGluCyArgProProProserPheSerTriP	180		
Dd	465 -----	465		
OY	181 ThrglyAlaAlaLeuSerSerGInglyThrLYsProThrThrSerHisPheSerValLeu	200		
Dd	466 -----GIGCTC	471		
OY	201 SerPheThrProArgProGlnAspHisAspThrasPleuThrcySHisValasPheSer	220		
Dd	472 AGCTTCACGCCACAGACCCCAGAGACACAACACCGACTCACCCTGATGGACTCTCC	531		
OY	221 ArgLYSGLYValSerAlaGInArgThrValArgcyleuArgValAlaTyrTrlaProArgasp	240		
Dd	532 AGAAAAGGTGTAGCGCCACAGAGAGACCGTCCGACTCGTGTGGCTATGCCCCCAAGAC	591		
OY	241 LeuValIIleSerILEserArgAspsnThrProAsp-	252		
Dd	592 CTGTGTATCAGCATTTCAAGTGAACAACAGCCAGCCCTGGAGCCCCAGGCCAGGGAAT	651		
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Dd	712 CAGCCCCCTGCCACTAGCTAGCTGGGTCCGTGCAAGACAGATGCTCTCTCTGTCCTCC	771		
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OY	252 -----	252		
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Db	952	AACCTGGGAACGGGACGCTCTCTCCAGTACTGGAGGGGCCAAAGCCTGTGGCTGTGTGT	1011
QY	291	ValThrHisSerSerProProAlaArgLeuSerThrThrGlnArgGlyGlnValLeuSer	310
Db	1012	GTCACACACACAGCCGCCCCAGCCAGAGGTGAGCTGAGCTGAGACCCAGAGGGGACAGGTTCTAGC	1071
QY	311	ProSerGlnProSerAspProGlyValLeuGlnLeuLeuLeuProArgValGlnValGlnHisGln	330
Db	1072	CCCTCCAGCCCTCAGACCCCGGGGGCTCTGGAGCTGGCTGGCTGGGTTTCAAGTGGAGCAGAA	1131
QY	331	GlyGlnPheThrCysSHisAlaArgHisProLeuGlnGlySerGlnHisValSerLeuSerLeu	350
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QY	351	SerValHisThrLysThrLysGlyLeuLeuSerThrAlaPheSerAsnGlyAlaPheLeuGly	370
Db	1192	TCCGTGGCACTTAAGAAAGGACTATCTCAACGGCATTTCTCAACGGAGGCTTTCTGGGA	1251
QY	371	IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro	390
Db	1252	ATCGGCATCAGCGGCTCTTCTTCTCTCTGCTGCTGGCCCTGATCATCATGAAAGATTCTACCG	1311
QY	391	LysArgArgThrGlnGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu	410
Db	1312	AAGAGACGGACTCAGACAGAAACCCAGAGGCCAGGTTCTCCGGCACAGCAGCATCTGT	1371
QY	411	AspThrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla	430
Db	1372	GATTACATCATGTGGTCCGACGGCTGGGCCCTGGCTCAGAAAGCGAATTCAGAAAGCC	1431
QY	431	ThrProAsnSerProAlaGlyThrProLeuProProGlyAlaProSerProGlnSerLysLys	450
Db	1432	ACACCAACACATCTCTCGACCCCTCTCCACAGAGTCTCTCTCCAGATCAAAAGAAAG	1491
QY	451	AsnGlnLysLysGlnThrGlnLeuProSerPheProGlnProLysSerSerThrGlnAla	470
Db	1492	AACCAAGAAAAGCAGTATCAGTTGCCACGATTTCCCAAGACCAACCATCATCTCCACTCAAGCC	1551
QY	471	ProGlnSerGlnGlnSerGlnGlnGlnLeuHisThrAlaThrLeuAsnPheProGlyVal	490
Db	1552	CCAAATATCCCGGAGAGACCAAGAGAGACTCCATATATCCAGCTCAACTTCCAGGGGCTC	1611
QY	491	ArgProArgProGlnAlaArgMetProLysGlyThrGlnAlaAspThrAlaGlnValLys	510
Db	1612	AGACCCAGGCGCTGAGGCCCGGATGATCCCAAGGGCACCCAGGCGGATTGTGCAGAAAGTCAAG	1671
QY	511	PheGln 512	
Db	1672	TTTCAA 1677	
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XX	ABX97802;		
XX	AC		
XX	16-MAY-2003	(first entry)	
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XX	XX		
KW	Human; PRO; gene; ss; cytosstatic; chromosome mapping; gene mapping;		
KW	protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;		
KW	chondrocyte differentiation; chondrocyte proliferation; tumour.		
XX	OS	Homo sapiens.	
XX	XX		
XX	XX	US2003032102-A1.	

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PR	01-DEC-1998;	98MO-US25108.
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Db 1372 GATTACTCATATGTGGTCCGACGGCTGGCCCTGGCTGACAGCGGAATCAGAAAGCC 1431
Oy 431 ThrProAsnSerProArGThrProLeuProGlyAlaProSerProGlnSerLys 450
Db 1432 ACACCAAAAGCTCTCGGACCCCTCCCTCCACCAAGGTCCTCCCTCCAGATCAAGAAC 1491
Oy 451 AsnGlnLysLysGlnLysGlnLeuProSerPheProGlnProLysSerSerThrGlnAla 470
Db 1492 AACACGAAAAAGCATCATGTTGCCAGCTTCCCAACCAATCATCTCACCACAGCC 1551
Oy 471 ProGlnSerGlnLysSerGlnLysGlnLysHisTyrAlaThrLeuAsnPheProGlyVal 490
Db 1552 CCAAGATCCCAAGAGAGACCAAGAGAGACTTCATTTATGCCAGCTCACTTCCAGGCGCTC 1611
Oy 491 ArgProArGProGlnAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
Db 1612 AGACCCAGCGCTGAGGCCGAGATGCCCAAGGGACCGGATTTATGCAGAAAGTCAAG 1671
Oy 511 PheGln 512
Db 1672 TTCCAA 1677
RESULT 14
ABX78586
ID ABX78586 standard; cDNA: 2764 BP.
AC ABX78586;
AT 15-APR-2003 (first entry)
DT 15-APR-2003
XX Human PRO polynucleotide #59.
DE
XX
KW Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;
KM liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;
XX antibody-dependent enzyme mediated prodruug therapy.
OS Homo sapiens.
XX
XX US2003027272-A1.
PN
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-0176492.
XX
XX 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US0505190.
PR 14-MAY-1999; 99WO-US10793.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28233.
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PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
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PR 22-FEB-2000; 2000WO-US04344.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.
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PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
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PR 01-DEC-2000; 2000WO-US34956.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
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PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
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QY 252 ----- 252
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QY 252 ----- 252
Db 712 CAGCCCCCTGCCACTGAGCTGGTCTGTCAGAGACAGAGTCTCTCTGTCATCCC 771
QY 252 ----- 252
Db 772 TGGGGCCCTAGACCCTGGGGCTGGAGCTCCCGGGGTGAAGCTGGGATTCAGGGCGC 831
QY 252 ----- 252
Db 832 TACACCTGCCAGCGGAGACAGGCTTGCTCCAGACGGAGCCCTGACCTCTCTGTG 891
QY 253 ----- ProProGluSerGlnLeuArgValMetValSerGlnAlaSerArgThrValLeuGlu 270
Db 892 CAGTATCTCTCAGAGAACCTGAGAGTGTGTTCCCAACCAACAGGACAGTCTGGAA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyInSerLeuCysValCys 290
Db 952 AACCTTGGAGACGGCAGCTCTTCCAGTACTGGAGGCCCCAAAGCTGTGCTGTCTGT 1011
QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlnValLeuSer 310
Db 1012 GTCCACACAGCAGACCCCGCCAGCGCTGAGCTGGACCCAGAGGGGACAGTTCAGC 1071
QY 311 ProSerGlnProSerSerProGlyValLeuGlnLeuProArgValGlnValGlnHisGlu 330
Db 1072 CCTCCACAGCCTCAACACCCGGGGGTCCTGGAGCTGTGGGTTCAAGTGGAGCAGAA 1131
QY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
Db 1132 GAGAGATTCACTGCTGCCACGCTGGCACCCACTGGCTCCACAGACGCTCTCTCAGCTCTC 1191
QY 351 SerValHisArgTrpLysArgLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
Db 1192 TCCGTGCACATTAAGAAAGGACATCATCTCAAGGCAATTCACAAGGAGGGTTCTGGGA 1251
QY 371 IleGlyTyrLeuThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390
Db 1252 ATGGGATCAGGGCTCTTCTTTCTCTGCTGCTGCTGATCATCAAGAAATTCATCCG 1311
QY 391 LysArgArgThrGlnThrGlnIuThrProArgProArgPheSerArgHisSerThrIleLeu 410
Db 1312 AAGAGACGAGCTCAGACAGAAACCCGAGGCCAGGTTCTCCGGCACACAGCATCTTG 1371
QY 411 AspTyrTleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
Db 1372 GATTACATCAATGTGGTCCCGAGGGCTGGCCCCCTGGCTCAGAAAGCGAATTCAGAAAGCC 1431
QY 431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys 450
Db 1432 ACACCAAAACAGTCTCTGGAGACCCCTCTCCACCAAGGTGCTCTCCCAAGATCAAGAGAG 1491
QY 451 AsnGlnLysGlnGlnTrpGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
Db 1492 AACCAAGAAAAGAGTATCATGTGCCCCAGTTTCCCAAGAACCCAAATCATCCACTCAAGCC 1551
QY 471 ProGluSerGlnGluSerGlnGluLeuHisTyrAlaThrLeuAsnPheProGlyVal 490
Db 1552 CCAAGATCCCAAGAGAGCCAAAGAGAGTCAATTAAGCCAGCTCAACTCCCAAGGGCTC 1611
QY 491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
Db 1612 AGACCCAGGCTGAGGGCCGATGATGCCAAGGACACCCAGCGGATTAATGCAAGAGTCAAG 1671
QY 511 PheGln 512
Db 1672 TTCCAA 1677

RESULT 15

ABX75599
ID ABX75599 standard; cDNA; 2764 BP.
XX
AC ABX75599;
XX
DT 26-MAR-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein, PRO940.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW antithrombotic; vulnereary; tumour necrosis factor-alpha;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; arthritis; sports injury.
XX
OS Homo sapiens.
XX
PN US2003022298-A1.
XX
PD 30-JAN-2003.
XX
PE 20-JUN-2002; 200205-0176913.
XX
PR 05-NOV-1997; 97WO-US20069.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
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PR 13-SEP-1999; 99WO-US20944.
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PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
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PR 30-NOV-1999; 99WO-US28409.
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PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
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PR 11-FEB-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US04341.
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PR 24-FEB-2000; 2000WO-US05004.
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PR 02-MAR-2000; 2000WO-US05841.
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PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07552.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000MO-US1404Z.
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PR 02-JUN-2000; 2000MO-US15264.
PR 28-JUL-2000; 2000MO-US20710.
PR 11-AUG-2000; 2000MO-US22031.
PR 23-AUG-2000; 2000MO-US23522.
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PR 08-NOV-2000; 2000MO-US30952.
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PR 29-JUN-2001; 2001MO-US21066.
PR 09-JUL-2001; 2001MO-US21735.
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PR 31-MAR-1998; 98US-080194P.
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PR 26-JUN-1998; 98US-090863P.

Alignment Scores:

Pred. No.: 2,54e-153 Length: 2764
Score: 2265.00 Matches: 450
Percent Similarity: 74.92% Conservative: 1
Best Local Similarity: 74.75% Mismatches: 3
Query Match: 83.70% Indels: 148
DB: 25 Gaps: 2

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DB 46 ATGCTACTGCACGCTGCTGCTCCGCTGCGGCGGCTCCACGAGCTATGATGGAGGA 105
QY 21 PherPrlLeuArgValGlnGluSerValMetValProGlnGlyLeuCysIleSerValPro 40
DB 106 TTCTGGATACGAGTGCAGGAGTCACTGATGGTCCGAGGCGCTGTGTCATCTCTGTGCC 165

QY 41 CysSerPheSerThrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyr 60
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 Db 166 TGTCTTTCTCTCAACCCGACAGACTGGACAGGGCTTACCCAGCTTATGGCTACTGG 225
 QY 61 PheLysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
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 Db 226 TTCAAAGCAGTGTGACGACCAACCAAGGGGTCTCGGTGGCCACAAACCAAGAGTGA 285
 QY 81 GluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
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 Db 286 GAGGTGGAATGAGCACCCTGGGGCCGATTCACACTGCGGGATCCCGCAAGGGGGAAC 345
 QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
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 Db 346 TGTCTCTGTGTGATCAGACGCGCGCATGACAGATGATGACACAGTACTTCTTGGGGT 405
 QY 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
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 Db 406 GAGAGAGGAAGCTATGTGACATATTAATTTTCATGACGATGGTCTTTTAAAGTACAA 465
 QY 141 AlaLeuThrGlnLysProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal 160
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 QY 161 ThrValIleCysValPheAsnTrpAlaPheGlnGluCysProProPheSerPheSerTrp 180
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 Db 465 ----- 465
 QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
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 Db 472 AGGTTTCAAGCCAGACCCGACGACACACACGACGACCTCAGCTTGGGACTTCTCC 531
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 Db 532 AGAAAGGCTGTGAGCGACAGAGAGACCGTCCGACTCGGTGGCTATGCCCCAGAGAC 591
 QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
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 Db 592 CTGTGTATCAGCATTTTCACGTGACACACGACCGCTGGAGCCCCAGCCCCAGGAAT 651
 QY 252 ----- 252
 Db 652 GTCCCATACCTGGAAGCCCAAAAGGCCAGTTCCTGCGGCTCCTGTGCTGCTGACAGC 711
 QY 252 ----- 252
 Db 712 CAGCCCCCTGCACACTGAGCTGGGTCTGTCGAGAAGAGTCTCTCTGTCCTCATCC 771
 QY 252 ----- 252
 Db 772 TGGGGCCCTAGACCCTGGGGCTGAGACTGCCGGGTGAAGGCTGGGATTCAGGGCGC 831
 QY 252 ----- 252
 Db 832 TACACCTGCGAGCGGAACAGGCTTGGCTCCACAGCAGGAGCCCTGGACTCTCTGTG 891
 QY 253 -----ProProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGln 270
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 Db 892 CAGATCTCTCCAGAGAACTGAGAGTATGTTTCCCAAGCAAAACAGACAGTCTCTGAA 951
 QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyGlnSerLeuCysLeuValCys 290
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 Db 952 AACCTTGGGAACGCGACGTCTCTCCAGTACTGGAGGGCCAAAGCCGTGCTGTGCTGT 1011
 QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
 |||||
 Db 1012 GTCACACAGACAGCCCCCAGGCTGAGTGGACCCAGAGGGGAGAGGTTCTGAGC 1071

QY 311 ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnIleGln 330
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 Db 1072 CCTCCAGAGCCCTCAGACACCCGGGGGTCTGTGAGCTGCTGGGTTCAGTGAAGAGCAAGAA 1131
 QY 331 GlyGlnPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
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 Db 1132 GGAGAGTTCACCTGCCACAGCTCGGACACCCACTGGGCTCCAGACAGCTCTCTCAGACCTC 1191
 QY 351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
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 Db 1192 TCCGTCCACTATTAAGAAAGGACATCTCAACGGCATTTCTCAACGAGCGTTTCTGGGA 1251
 QY 371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390
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 Db 1252 ATGGGATTCACGGCTCTTCTTTCTCTGCTGCTGGCTGCTGATCATCATGAAGATTCTAAC 1311
 QY 391 LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu 410
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 Db 1312 AAGAGACGCACTAGACAGAAACCCGAGGCCAGGTTCTCCCGCACACAGCATCTCTG 1371
 QY 411 AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
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 QY 431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlnSerLysLys 450
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 Db 1432 ACACCAAAACAGTCTCTCGAGACCCCTCTCCACAGAGTCTCTCCCGCAAGATCAAGAGAG 1491
 QY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGlnProLysSerSerThrGlnAla 470
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 QY 471 ProGlnSerGlnGlnSerGlnGlnGlnLeuHisTyrAlaThrLeuAsnPheProGlyVal 490
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 Db 1552 CCAGATCCCGAGAGAGCCCAAGAGAGACTCATTAATGACACGCTCAACTTCCAGAGGCTC 1611
 QY 491 ArgProArgProGlnAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGlnValLys 510
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 QY 511 PheGln 512
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 Db 1672 TTCCAA 1677

Search completed: October 8, 2003, 20:13:22
 Job time : 459 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:04:22 : Search time 3160 Seconds
(without alignments)
3937.940 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLLLSLGSGQAMDR.....RPEARMPKGTQADYAEVAFQ 512

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: em_gss_pro : *
25: em_gss_fod : *
26: em_gss_pnd : *
27: em_gss_vrl : *
28: gb_gss1 : *

29: gb_gss2 : *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1211.5	44.8	2017	11	AK042488 Mus muscu
2	1027.5	38.0	1201	13	BX345667 BX345667
3	1026.5	37.9	3939	11	AK036698 Mus muscu
4	927	34.3	1099	12	BM544297
5	895.5	33.1	876	13	BO711946
6	824.5	30.5	667	14	CB554607
7	789	29.2	514	2	BSM097253
8	734	27.1	1464	12	BSM544269
9	682.5	25.2	1060	12	BM925147
10	669.5	24.7	2478	11	AK087658
11	652	24.1	1745	12	BM906520
12	629	23.2	995	12	BM922784
13	621	22.9	1012	12	BM922958
14	619.5	22.9	997	12	BM921873
15	598.5	22.1	864	14	CB992313
16	597.5	22.1	936	10	BF663289
17	594.5	22.0	1201	13	BX39458
18	591.5	21.9	830	12	B1906741
19	587.5	21.7	1201	9	AL542696
20	570.5	21.1	888	14	CA495365
21	567.5	21.0	857	13	BO883649
22	560.5	20.7	1191	9	AL542471
23	556.5	20.6	916	12	B1910568
24	550	20.3	1714	11	BC030222
25	544	19.9	505	13	BX283650
26	538.5	19.9	1121	12	BM564074
27	538	19.8	871	12	B1518708
28	534.5	19.8	2220	11	BC035688
29	533.5	19.7	780	14	CB961761
30	533	19.7	934	12	BX324896
31	530.5	19.6	1001	12	BM561814
32	530.5	19.6	1071	12	BM920861
33	530	19.6	1793	11	AK046303
34	514.5	19.0	1049	13	BO072659
35	513	19.0	809	11	CB992745
36	508.5	18.8	2378	11	AK089205
37	493.5	18.2	1201	9	AL540764
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42	479	17.7	795	12	B1822428
43	468	17.3	510	12	BM483921
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ALIGNMENTS

RESULT 1	AK042488	2017 bp	mRNA	linear	HTC 05-DEC-2002
LOCUS	AK042488				
DEFINITION	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone: A630096C01 product: weakly similar to SLALC				
ACCESSION	AK042488				
VERSION	AK042488.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				

[illegible]

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Db      393 TTAGAGTGGGAAGCCCGAGGGGGCTTCCAGCTTGGGGATATCTCAAAAAGAACTGT 452
Qy      102 SerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnIleThrPheArgValGlu 121
Db      453 TCCTTGCTATCAAGATGTTTCAGTGGGAGAGCTCAACAACCTATTCTCCGGATGGAG 512
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Db      513 AGAGGA---TTGAGAGATTCAGTTTCAAGAGAGAG---TTCAGGCTCAAGATGGAAAGCC 566
Qy      142 LeuThrGlnLysProAspValIleProGluThrLeuGluProGlyGlnProValThr 161
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Qy      162 ValIleCysValPheAsnThrAlaPheGlnGluCysProProSerPheSerThrPhe 181
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Qy      182 GlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeuSer 201
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Qy      202 PheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSerArg 221
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Qy      252 ----- 252
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Qy      252 ----- 252
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Qy      253 -----Pro 253
Db      1101 CAAGCAGAGAAATAGCTGGGTCCCAAGCAACATACCTTGAGCTCTGTGCTGATACCC 1160
Qy      254 ProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlnAsnLeuGly 273
Db      1161 CCACAGGAGCTGAGAGTCTGTTTCCCAAGCAAGAGACAGTGTGGAAATCCCTCAGG 1220
Qy      274 AsnGlyThrSerLeuProValLeuGlnGlyInsLeuCysValLeuValCysValThrHis 293
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Qy      314 ProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnHisGlnGluLysPhe 333
Db      1341 TCTTGAAGACCTGGGGTCTCTGAGCTGCTCTGCTGTCACAGAAACATGAAAGAAATTC 1400
Qy      334 ThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeuSerValHis 353

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Db      1401 ACCTGTGCTGCACAGAACCCACTGGGTGCCAGCGCATCTCTGAGCCCTCTGTGCAC 1460
Qy      354 Tyr-----LysGlyLeu----- 358
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Qy      359 -----LleSer 360
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Qy      361 ThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCys 380
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Qy      401 ProArgPheSerArgHisSerThrIleLeuAspThrIleAsnValProThrAlaGly 420
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Qy      441 ProGlyAlaProSerPro 446
Db      1994 CCTGCACTCACTTCCC 2011

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RESULT 2
 LOCUS BX345667
 DEFINITION BX345667 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA clone CS01025YC24 5-PRIME, mRNA sequence.
 ACCESSION BX345667
 VERSION BX345667.1 GI:30373021
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by life technologies, a division of invitrogen. This sequence belongs to sequence cluster 9384.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0A1025B120P1c1cluster=9384.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0A1025B120P1.
 Location/Qualifiers
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 /organism="Homo sapiens"

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/Note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      262 a      333 c      339 g      228 t      39 others
ORIGIN

Alignment Scores:
Pred. No.:      3.38e-76      Length:      1201
Score:          1027.50      Matches:      211
Percent Similarity: 75.24%      Conservative: 26
Best Local Similarity: 66.98%      Mismatches: 61
Query Match:    37.97%      Indels:      19
DB:             13      Gaps:      1

US-09-937-636-3 (1-512) x BX345667 (1-1201)

QY      1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20
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      220 TTGCACCTCTCTACCCCGCGGATGCGTGGAGCACTACTGCTCTATGCTCTGCTGCT 279
      60 pPheIysAlaValIleGlnIleThrIleGlyAlaProValAlaThrAsnIleGlnSer 80
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      520 AGCCCTGACTAAGAGCGTATGTCATCTCCCGAAGACCTGGAGCCGCGGAGCGCGGT 579
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      819 CCTTATTATCAGCATTTTCATCATGACACAGC----- 849

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      300 userTrpThrGlnArgIleGlnIleuSerProSerGlnPro 314
      951 GAGCTGGGTCTT-GCAGGCGAGCTTCTCTCTGCTCCACCCC 992

RESULT 3
AK036698
LOCUS
DEFINITION
MUS MUSCULUS adult male bone cDNA, RIKEN full-length enriched
library, clone:98J0164H23 product:weakly similar to SLALC
ACID-BINDING LECTIN [Homo sapiens], full insert sequence.
ACCESSION
AK036698
VERSION
AK036698.1 GI:26331615
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakauchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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4 Kawaji, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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Pletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazza, R., Mombaur, P., Nordone, P.,
Rung, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
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and Hayashizaki, Y.

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QY 253 -----
Db 2492 GAGATAGGCTGGGCTCCACAGACATACCTGGACCTCTGTGTGTATACCCCAACAG 2551
QY 256 -----
Db 2552 GACCTGAGAGTACTGTTTCCCAAGCAAGACAGCATGTGGAAATCCTCAAGAAATGCC 2611
QY 276 -----
Db 2612 ATCTCCCTCCAGTCTCTGAGGGCCAAAGCTTGGCTTACTGTGTCTACCTTACCAAT 2671
QY 296 -----
Db 2672 CCCCAGCCAAATGTAGTTGGCTGGGTGACACAGACCTGTATCCAAATCCAGTCTCA 2731
QY 316 -----
Db 2732 GAGCCGTGGTCTGTGAGCTCTGTGTCTGTCAGAGAAATCAAGAGATTCACCTGT 2791
QY 336 -----
Db 2792 GCTGCACAGAACCATCTGGTGTGCCCAAGCATCTCTGTGAGCTCTGTGTGACCTGTGAG 2851
QY 355 -----
Db 2852 TAGGCAAAAGGACACTGGGATCTGTGATGAGGGCCAGCTGCTGACATTTCTCTCTC 2911
QY 356 -----
Db 2912 CACAGACCGCCCAAGATGTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2971
QY 357 -----
Db 2972 CAACCTGCTCTCCAGACCTGGGCTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3031
QY 358 -----
Db 3032 GCTGAGAGGAGAACAGACGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3091
QY 359 -----
Db 3092 GGTCAACAGCTCCCTGAGCTCTCTCAAGAGCTGGGGCCAGCTCTGCTCAAGCTGTGA 3151
QY 359 -----
Db 3152 GTCTGSAACACCATGAGACCCAGACCACTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 3211
QY 360 -----
Db 3212 TGCACAGCACTTCTCAAGGAGCAGTTTGGCTTGGCATCAGACCCCTCTCTCTCTCTCT 3271
QY 379 -----
Db 3272 GTGCCCTCATCTGTGTATCTGTGAAGACCTCTCAGAAAGAAAGAACCCAGAGGAGACCTC 3331

QY	3399	OARProArpgheserArghHhSserThrlleLeuAspTyrIleAsnValProThrAl	419
DB	3332	CAGGCCCAAGCTCTCCCGGGCAGCAGCATCTCTGACTACTCATATGGTCCCAAGAC	3391
QY	419	aglyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgrThrProLe	439
DB	3392	CAGGTCCCTGGCT-----CGAATTGGAAAGCTGAACACAGATGCCCTTCTAGAGAGCTC	3445
QY	439	wProProGlyAlaProSerProGluSerLysLysAsnGlnLys---LysGlnTyrGlnLe	458
DB	3446	ACCCCTGGACACCTCACTTCCTTAACCAAAAGAAAGAAAGAACCCACATTCACAGTA	3505
QY	458	wProSerPheProGluProLysSerSerThGlnAlaProGluSerGlnGlnSerGlnG	478
DB	3506	CCCTGGTTGCCACATGCCACATCATCTCTCAGGTCCCATCTCTGAGTAATACCCGA	3565
QY	478	UGLUeuhHstYrAlaThrLeuAsnPheProGlyValAlaArgProGluAlaArgMe	498
DB	3566	AGAACTCCACATCTGCTCTCAACTTCCTCCGCTGAGACTGAGC--GAGACCAGGA	3622
QY	498	tProLysGlyThrGlnAlaAspTyrAlaGlnLys	510
DB	3623	TCCCAAGACACACTATCTGTATTCACAGAGCTGAGA	3659
RESULT 4			
BMS44297			
LOCUS	BMS44297	1099 bp	mRNA linear EST 20-FEB-2002
DEFINITION	AGENCOURT_6490592 NIH_MGC_125 Homo sapiens CDNA clone IMAGE:5587803		
ACCESSION	BMS44297		
VERSION	BMS44297.1	GI:18775435	
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1099)		
JOURNAL	NIH-MGC http://mgs.ccl.nh.gov/.		
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgarbbs@femail.nih.gov Tissue Procurement: Invitrogen CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL12357 row: 0 column: 04 High quality sequence stop: 725.		
FEATURES			
SOURCE			
	1..1099		
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	/clone="IMAGE:5587803"		
	/lab_host="DH10B"		
	/clone_11b="NIH_MGC_125"		
	/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."		
BASE COUNT	225 a	360 c	283 g
ORIGIN			230 t
			1 others

Pred. No.:	8.8e-68	Length:	1099
Score:	927.00	Matches:	206
Percent Similarity:	63.788	Conservative:	30
Best Local Similarity:	55.688	Mismatches:	67
Query Match:	34.26%	Indels:	67
DB:	12	Gaps:	8

US-09-937-636-3 (1-512) x BM544297 (1-1099)

QY	1	MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaIleMetAspGlyArg	20
DB	45	CTGCTGCTGCCCCCTGCTGCTGCTGCGCCGTCGGGGGCGGGGCTCCGTGACAAAGATCCAGT	104
QY	21	PheTrpIleArgValGlnGlnuSerValMetValProGlnGlnGlyLeuCysIleSerValPro	40
DB	105	TACAGCTTCAAGTCGACGAGACGACGAGTGGCCGGGTCGGAGGGCTGTGTATCGTCT	164
QY	41	CysSerPheSerTrpProArgGlnAspTrpThrGlySerTrpProAlaTrpGlyTrp	60
DB	165	TGCACCTCTCCATACCCCGGGATGGCTGGGACGAGTCTACGTCGCTTATGGCTACGG	224
QY	61	PheIysAlaValThrGlnuThrThrIlyGlnGlyAlaProValAlaThrAsnHisGlnSerArg	80
DB	225	TTCAAGACGACGACCCGACCCAAAGACGGGTGCTCTGTGGCCATCAACACAGATCGA	284
QY	81	GluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaGlyAsn	100
DB	285	GAGGTGCATGAGCACCCGGGACCGATTCACGCTCATCGGGGATCCCGCAAGGAGC	344
QY	101	CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTrpPheArgVal	120
DB	345	TGCTCTTGCTGATCAGACGCGGCGAGAGGAGATGAGGATGTACTTCTTCGGGTG	404
QY	121	GluArgGlySerTrpValArgTrpAsnPheMetAsnAspGlyPhePheLeuIlyValThr	144
DB	405	GAGGAGAGAACCGCTGTGACATATCTTCCGACCAATGCGTTCTTCTTAAAGTAAACA	464
QY	141	AlaLeuThrGlnTrpProAspValTrpIleProGlnuThrLeuGlnProGlyAlaProVal	160
DB	465	GCCTGATCTGAGAAAGCTGATGTCTCATCCCGAGACCGCTGGACCGGGGACCGGTG	524
QY	161	ThrValIleCysValPheAsnTrpAlaPheGlnGlyCysProProPheSerPheSerTrp	180
DB	525	ACGGTCATCTGTGTGTTAACTGGGCTTCAAGAAATGTCAGCCCTCTTCTCTCGTG	584
QY	181	ThrGlyAlaIleLeuSerGlnGlyTrpIlyTrpProThrSerHisPheSerValLeu	200
DB	585	ACGGGGCTCCCTCTCCCTCAAGAAACCAACACAGACGCTCCCACTTCTCAAGTCTC	644
QY	201	SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	220
DB	645	AGCTTCACGCCAGCCCCCAGGACACGACACCGACCTCAGTGGCATGTGGACTTCC	704
QY	221	ArgIlyGlyValSerAlaGlnArgThrValArgLeuArgValAlaTrpAlaProArgAs	240
DB	705	AGAAAGGGTGTGAGCCACAGAGAGACGCTCCGAGATCCGTGTGGCC	764
QY	240	PheValIleSerIleSerArgAspAsnThrProAspProProGlnAsnLeuAlaValIle	260
DB	750	-----	750
QY	260	tValSerGlnAlaAsnArgThrValLeuGlnAsnLeuGlyAsnGlyThrSerLeuProVa	280
DB	751	-----TCCCTGGAATCCAGGAAC-----GTCAT	778
QY	280	IleuGlnGlyGlnSer-----LeuCysLeuValCysValThrHisSe	294
DB	777	ATATTGGAAGATCGAAGAAAGCCCTTCGCGGCTCCTGTGGGCTGCTGACG---CC	833
QY	294	rSerProProAlaArgLeuSerTrpThr---GlnArgGlyGlnValLeuSerPro---	311
DB	834	CAGCCCCCGCCCGTGTAGCTGTGGTCTCTGCCAGGCAAAATGCTTCTTCTCTCGCA	893

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QY 312 --SerGlnPro-SerAspPro-----GlyValLeuGluLeuPro 323
Db 894 TCCAAACCCCTGGGGGATCCCCCTAAACCCCTTGGGGCCACTTAACCTTACTCTGCATACCA 953
QY 324 ArgValGlnValGluHis-----GluGlyGlu 332
Db 954 AAATGTTTCTGGCGCCATTTATCCGGCTTCATAAACACACTCCCATCAGTCTCAGACT 1013
QY 333 PheThrCysHisAlaArgHisPro 340
Db 1014 CACAGCTGCTATCAATATATACCT 1037

RESULT 5
BQ711946 876 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_7977108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215765
DEFINITION 5', mRNA sequence.
ACCESSION BQ711946
VERSION BQ711946.1 GI:21850845
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsd-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.nih.gov
Plate: LICM2385 row: d column: 06
High quality sequence stop: 685.
FEATURES
source
location/Qualifiers
1..876
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6215765"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
BASE COUNT 176 a 304 c 244 g 151 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2 97e-65 Length: 876
Score: 895.50 Matches: 190
Percent Similarity: 65.19% Conservative: 1
Best Local Similarity: 64.85% Mismatches: 4
Query Match: 33.09% Indels: 98
DB: 13 Gaps: 1
US-09-937-636-3 (1-512) x BQ711946 (1-876)
QY 260 MetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuPro 279
Db 2 ATGGTTTCCCAAGCAACAGACAGCTCCGGAAGAAACCTTGGGCAACGCACTCTCCCA 61
QY 280 ValLeuGluGlyGlnSerLeuCysValThrHisSerProProAlaArg 299

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Db 62 GTACTGAGGAGCCAAAGCCTGTGCTGTGTCTGCACACAGACAGCCCCCAGCCAGG 121
QY 300 LeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyVal 319
Db 122 CTGAGCTGAGACCCAGAGGGGAGGTTCTAGCCCCCTCCAGCCCTAGACCCCGGGGTC 181
QY 320 LeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArgHis 339
Db 182 CTGAGCTGCGCTCGGCTTCAAGTGAGCAGCAAGAGAGATTCACTCCACGCTCGGCAC 241
QY 340 ProLeuGlySerGlnHisValSerLeuSerValHisTrp----- 354
Db 242 CCACTGGGCTCCAGACAGCTCTCTCTAGCTCTCGTGCATCTCCCGAAGCTGCTG 301
QY 354 ----- 354
Db 302 GGCCCTCTCTGCTCTGGAGGCTGAGGGTCTGCACACTGCAGCTCTCTCCAGGCCAGC 361
QY 354 ----- 354
Db 362 CCGGCCCTCTCTGCGCTGTGTGGGAGAGCTGTGAGGGGAACAGACAGCAG 421
QY 354 ----- 354
Db 422 GACTCTTGAGGTACACCCCACTAGCCGGGCGCTGGGCCAACAGCTCTGAGCTTC 481
QY 354 ----- 354
Db 482 CATGAGAGGCTACGTCCTCGGCTCAGGCTCCGCTGTGAGGCTGGAACGTCTATGGGGCC 541
QY 355 ----- 355
Db 542 CAGAGTGATCCATCTCTGAGCTGCCAGATAAAGAGGACTATCTCAACGGCATTCCTCC 601
QY 365 AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIle 384
Db 602 AAGGAGCGCTTGTGGGATCGGCATCAGCGCTCTCTTCTCTGCTGCGCTGCGCTGATC 661
QY 385 IleMetLysIleLeuProLysArgArgThrGlnThrGluThrProArgProArgPheSer 404
Db 662 ATCATGAAATCTTACCGAAGAGACGAGCTGACAGCAAAACCCGAGGCTCTCTCC 721
QY 405 ArgHisSerThrIleLeuAspTrpIleAsnValAlaProThrAlaGlyProLeuAlaGln 424
Db 722 CGGCACAGACGATCTCTGATTCATCATATGTGTCCGACGCTGGCCCTGGGCTCAG 781
QY 425 LysArgAsnGlnLysAlaThrProAsnSerPro-ArgThrProLeuProGlyAla-- 443
Db 782 AAGCGAATCAAAAGCCACACCAAAACAGTCTTGGAGCCCTCTCCAAAGGTGGCTC 841
QY 444 ProSerProGluSerLysLysAsnGlnLysLys 454
Db 842 CCNTCCCGGAATCCAAAGAGAACCCGCAAAA 874

RESULT 6
CB554607 667 bp mRNA linear EST 01-JUN-2003
LOCUS MMSF0040_D05 MMSF Macaca mulatta cDNA, mRNA sequence.
ACCESSION CB554607
VERSION CB554607.1 GI:31303802
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 667)
AUTHORS Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
TITLE Expressed sequence tags from Rhesus macaque spleen
JOURNAL Unpublished
COMMENT Contact: Holzman T

```

Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: tedelocke@u.washington.edu

Similar to GenBank entry AF311905 AF311905 Homo sapiens static
acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
8/2001

Plate: MMS0040 row: D column: 05.

FEATURES

source

Location/Qualifiers

1..667

/organism="Macaca mulatta"

/mol_type="mRNA"

/db_xref="taxon:9544"

/sex="male"

/cell_type="monocytes"

/dev_stage="adult"

/clone_lib="MMS"

/note="Organ: spleen"

BASE COUNT

165 a 217 c 145 g 140 t

ORIGIN

Alignment Scores:

Pred. No.:	2e-59	Length:	667
Score:	824.50	Matches:	162
Percent Similarity:	93.82%	Conservative:	5
Best Local Similarity:	91.01%	Mismatches:	10
Query Match:	30.47%	Indels:	1
DB:	14	Gaps:	1

US-09-937-636-3 (1-512) x CBS54607 (1-667)

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QY 336 HSA1AAGHSPLEUGLISERLHISVALSERLEUSERLEUSERVALLHISTYRYS 355
DB 1 CACGCTCAGACACCCCTGGTCTCAGACGCTCTCTCAGCCTCTCCCTGCATTAAG 60
QY 356 LYSGLYLEU1LESETHTHALPHERASNGLYALPHELEUGLYLLEGLY1LEHRA 375
DB 61 AAGGACTCATCTCAACGGCATTCACAGGAGGTTCTTGGAATCGCATCAAGGCT 120
QY 376 LEULEPHELEUCYSEU1ALEU1LEU1LEU1LEU1LEU1LEU1LEU1LEU1LEU1 395
DB 121 CTCTTTTCTCTGCTCCTCAGCCTGATCATGAGATTCATCAAGAGACAGACTCG 180
QY 396 THRGLUHPROARHPROARHPROARHPROARHPROARHPROARHPROARHPRO 415
DB 181 GCAGATACCCCAAGGCCAGGCTTCGCCGACACAGCATCTCGATTAATCAATGTG 240
QY 416 VALPROTHRALAGLPROLEU1AGL1NLYSARGASNG1NLYSALATHPROHNSER 435
DB 241 GTCCCGAAGGCCGCCCTGGCTGCTCAATCGAATCAAGAAAGCCACACCAAGCATCT 300
QY 436 --AAGTHPROLEU1PROGL1YALPROSER1PROGL1YALPROSER1LYSANG1N 454
DB 301 TCTCGGACCCCTCTCTCCACACAGTCTCTCTCTCCACAGATCAAGAAAGAAAAAG 360
QY 455 G1N1YRG1NLEUPROSER1PHEPROGL1UPROLYS1SER1THG1NALAPROGL 474
DB 361 CAGCATACAGTTCCAGATTCCACAGAACCAATATGATCACTCAAGCCCAAGATCC 420
QY 475 GLUSERGLNGL1NLEU1HIS1YRALATPHE1LEU1ANPHE1PROGL1YALARG 494
DB 421 GAGACCCCAAGAGACCTCCATTAATGACAGGCTCACTCCAGGCGTCCAGCCAG 480
QY 495 GUAAATARGMECPROLYSG1YTHRG1NALAASPTYRALAG1VALYSPHEGLN 512
DB 481 GAGGCGTGGATGCCCAAGGACACCAAGCGGATTAACGAGAAATCAAGTTCCA 534

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RESULT 7
HSM097253
ID HSM097253 standard; RNA; EST; 514 BP.
XX

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AC BX470328;
XX SV BX470328.1
XX DT 09-MAY-2003 (Rel. 75, Created)
XX DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX DE Homo sapiens mRNA, EST DKFZp79N169_r1 (from clone DKFZp79N169)
XX EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX RN [1]
XX RP 1-514
XX RA Bloecher H., Boecher M., Mewes H.W., Well B., Amlid C., Osanger A., Fobo G.,
XX RA Han M., Wiemann S.;
XX RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
XX RL WFS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX
XX This is the 5' sequence of the clone insert
XX CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
XX CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
XX CC sequenced by GBF (National Research Centre for Biotechnology
XX CC Ltd., Braunschweig/Germany) within the cDNA sequencing
XX CC consortium of the German Genome Project.
XX CC No sl sequence available.
XX CC This clone (DKFZp79N169) is available at the RZPD in Berlin.
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
XX CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
XX FH 1..514
XX FT /db_xref="taxon:9606"
XX FT /mol_type="mRNA"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp79N169"
XX FT /clone_lib="779 (synonym: hnccl). Vector pSport1_sfl; host
XX FT DH10B; sites SfiI + SfiIB"
XX FT /dev_stage="fetal"
XX FT /tissue_type="liver"
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XX SQ Sequence 514 BP; 115 A; 138 C; 152 G; 109 T; 0 other;
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XX Alignment Scores:
XX Pred. No.: 1.4e-56 Length: 514
XX Score: 789.00 Matches: 149
XX Percent Similarity: 99.33% Conservative: 0
XX Best Local Similarity: 99.33% Mismatches: 1
XX Query Match: 29.16% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-937-636-3 (1-512) x HSM097253 (1-514)
QY 1 MELLEULEPROLEU1LEU1LEU1SER1LEU1GLY1SER1G1NALAME1ASGLYARG 20
DB 63 ATGCTAATCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
QY 21 PHE1P1LEARGVALG1NGL1SERVAL1METVAL1PROGL1YLEUCYS1LESERVAL1 40
DB 123 TCTCGGATACGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAG 182
QY 41 CYSER1PHE1SER1Y1PROARGL1N1SP1P1N1Y1SER1TH1PRO1ARGL1Y1TTP 60
DB 183 TGTCTTTCTCTACCCCGGACAGACGCTGACAGGCTGCTACCCCACTTATGCTACT 242
QY 61 PHE1Y1A1AVAL1TH1GL1U1TH1Y1SG1Y1A1A1A1A1A1A1A1A1A1A1A1A1 80
DB 243 TTCACAGAGTGTGACAGACCAACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302

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Oy		339	ISpProlauGlySerClnHlSvlsSerleuSerleuSevalHlStylLyslysGlyLeuI	359
Dd		933	 ACCCCATATCCGGTTTCCACCCCGCTTAATCC-----	964
Oy		359	IeSerThrAlaPhseSerAsnGlyAlaPhelueGlyIleGlyIleThralaleu----	377
Dd		965	 -----TCCTTAGCCCTGTGGCCCCCTATGCCCTATATCCCCTTTTGTAACC	1010
Oy		378	----PheLeuCysLeuAlaLeuIlelleMetllsileLeuProLyArGrThrgInt	396
Dd		1011	 CCTTTTTCATTGTCTTAACCTCCCTATMAAAAGCTGTATACACAAGCATCTCA	1070
Oy		396	hrgUthrPro-----ArgProAqPhseSerArghIsSerThri	409
Dd		1071	 CACATACACCGGTTTATATACCCCTTTTGGCGTCCACCGCATTCGAC-----	1124
Oy		409	IeLeuAspTyrlIleAsnValValPrOthrAlaglyProLeuAlaGlnLysArasnGlnI	429
Dd		1125	 TTTCG-----CTTAACACCG	1139
Oy		429	ySalathrProAsnSerProArgrThrProglYalaPro-----	444
Dd		1140	 ACACACACACCGTAATGCACACCNCGCCCTATTCCTTATCCCTTCCTATAACA	1199
Oy		445	-----SerProGluserylLysAlasngInLysysG	455
Dd		1200	CTCATTTGTATATCACACCCCAACATACTTCCCTGGGGTCCNTTCTCCCCCTAACCTCC	1259
Oy		455	InTrygInLeuProSerPheProgluProLysSerSerThrgInAlaProgluserng	475
Dd		1260	::: GTANTAAACCGCCATTCACACCCCGGATTAATAATAC-AGCGTCCGCCCAAAATACACAC	1318
Oy		475	IuSerGInGUgluLeuHlStylAlaThrlEuasnPhreProglyAlarGrProArProg	495
Dd		1319	 CTTCC-----CANCGCTGAATTTCCCCACACCCCC	1348
Oy		495	IuaIaArGrMeProLys	500
Dd		1349	 CCATTTTATTCGCGGT	1365
RESULT 9				
Bm925147			1060 bp	mRNA
LOCUS				linear EST 12-MAR-2002
DEFINITION			AGENCOURT 5627330 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762452	
ACCESSION			5', mRNA sequence.	
VERSION			Bm925147	
KEYWORDS			Bm925147.1 GI:19375526	
SOURCE			EST.	
ORGANISM			Homo sapiens (human)	
AUTHORS			Homo sapiens	
TITLE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
JOURNAL			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
COMMENT			NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.lnl.gov Plate: LHAM12812 row: 1 column: 05 High quality sequence stop: 725. Location/Qualifiers 1..1060 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"	

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/clone="IMAGE.5762452"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: PCMV-SPORT6; Site_1: NotCl; Site_2: ECoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
BASE COUNT      235 a       336 c       284 g       202 t          3 others
ORIGIN

Alignment Scores:
Pred. No.:      3.3e-47      Length:      1060
Score:         682.50      Matches:     156
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US-09-937-636-3 (1-512) x BM925147 (1-1060)

QY 49 AsprTrphrIglySerThrProAlaArglyTyrrTriPhelySaLaValThrgluThrThr 68
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12 GATTACCTCGGCGCCAGTA---GTTCATGGCTACTGTTCCGGGAAGGGGCCAATACAGAC 68
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QY 69 LysglAlaProvalAlaThrAsnHisGlnSerArggluValGlumetSerThrargly 88
::: |||::: |||::: |||::: |||
69 CAGAGTGCTCAGGTGGCCCAACAACCACCTCGCGGAGTGGGAGAGACTCGGGAC 128
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QY 89 ArpphesInleuthrThgIyAspProAlaySglaySncysserIeuValIlleaRaspla 108
|||::: |||
129 CGATTCCACCTCTTGGGGACCATATCCAGAATTTACCTGAGCATGAGAAATCCC 188
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QY 109 GlumetGlnaSpGluSerGlnTyrrPhepheArGValGIuArglySerTyrrValArtyr 128
::: |||::: |||::: |||::: |||
189 AGAAGAACTGATGCGCGGAGATACTCTTCTTGATGAGAAAGAAAGT---ATAAATGG 245
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QY 129 AsnpHemetaSnaspGlyPhepheLeuLySValThrAlaleuthrGlnLysProkspyl 148
::: |||::: |||::: |||::: |||
246 AATTATTAACATCACCGGCTCTGTGTGAATGTGACAGCCTTGACCACAGGCCCAACATC 305
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QY 149 TyrllePrOgluThrLeugluPrOglylInProvalThrvallllecySValPheasnTrp 168
||||| ||||| ||||| ||||| |||||
306 CTCATGCCAGGACCCCTGAGTCCGGCGGCCGCCAGAAATCGACCTGTCTGTGCCCTGG 365
|||::: |||

QY 169 AlaphnegluglucyProProSerSerPheSerThrThrglyAlaAlaLeuSerSergIn 188
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366 GCCTGTGAGGAGGGACACCCCTTATATCTCTCGATAGGAGACTCCGTCCCC--- 422
|||::: |||

QY 189 GlyThrIryLysProThrThrSerHisPheSerValleuSerPheThrProARpProGlnASP 208
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423 ---CTGAGACCCCTCCACACCCCGCTCTCGGTGGTCCACCCATATCCACAGCCCGAGGAC 479
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QY 209 HisapThrApLeuThrCyHisHisAlaspheserArglySglYalSerAlaGlnArg 228
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480 CATGGCACCACTTCATCTGTCAGTGACCTTCCCTGGGGCCAGCGTAGCCAGCAAGAACAG 539
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QY 229 ThrValArgLeuArgValAlaTyrrAlaProArGaspLeuValIlleSerIlleserfargasp 248
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540 ACCGTCATCTCMACGTCTCTAC----- 563
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QY 249 AsnThrProAspProGluLysLeuArgValMetValSerGlnAlaAsnArgThrVal 268
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564 -----CCGCTCTCAAGAACTTGACCATATGACTGCTTCCAAGAGAGCGGACAGTA 611
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QY 269 LeuGluAsnLeuGlyAsnGlyThrseryleuProvalLeuGluGlyGlnSerLeuCySleu 288
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612 TCACACAGTCTGGGAAAAGGCTCATCTCTGTGCACATCCAGAGGGCCAAATCTCTCGGCTG 671
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Kuehl, P., Lewis, S., Matsuo, Y., Ntkaido, I., Pesole, G., Quackenbush, J., Schmitt, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bul, C., Fletcher, J., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofman, M., Hunne, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Nordone, P., Raring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokata, K., Wang, K.H., Weitz, C., Whittaker, C., Wilmberg, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kottuski, S. and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 21085660
 11217851

The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2478)

Agedchi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Onno, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takekida, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp).
 URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedic Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: <http://genome.gsc.riken.go.jp/>
 URL: <http://fantom.gsc.riken.go.jp/>
 Location/Qualifiers

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 DB 204 GGGTGGCTGGCTGACGACGGT---TATTCGCTCTGACTGACTGCTGCTCAGGAGAACGTGCAC 260
 QY 33 GLUGLYLEUCYSILLESERVALPROCYSSERPHESERTYRPROARGLINSPTPRHGLY 52
 DB 261 GAGGGCGCTGGCTCTTGTGTAGCTGCCAAGTCACAGTACCC-----AAATTC 308
 QY 53 SETRHPROALETYRCLYTYRTPRHELYSALAVALTHGLUHTHRILYSGILALAPRO 72
 DB 309 AAGAGCTGCTGTGGTGGTACTGGTTCGGGAGGGGCCCAATATATTACGGCGCTGCCA 368
 QY 73 VALALATHASNHTSGINSERARGLUVALGLUMETSETRHARGGLYARGPHEGLINLEU 92
 DB 369 GTGGCTACAAATGACCCACAGCATGACTGACAGAAAGCTCAGAGTGCATCTATCTC 428
 QY 93 THRGLYAPPROALALYSGLYANCYSERLEUVALILEARGASPLAELINMETGLINASP 112
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 DB 489 ACAGGAGCTACTCTTCTCAGATTGGAT---GGTTC---GTGAATACAGTTTTCAGAAC 542
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 QY 153 THRLEUGLUPROGLIYNPROVALTHRVALLIACYVALPHEASNTPRALAPHEGLINLEU 172
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 QY 173 CYSPROPROSERPHESERTPRHRLGLYALAALAULEUSERSERGLINGLYTHRILYSPRO 192
 DB 663 GGGACACCCCCCATCTTTCTCTGGATGATGATCGCCCTCCTCCCTGGGCCACAGAGACC 722
 QY 193 THRTHSERHNSPHESEVALLEUSERPHEHTHPRQARGPROGLINASPHISAPHTHASP 212
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 QY 213 LEUTHCYSHISVALASPHESERARGLYVALSERVALAGLINARGHTRVALARGLEU 232
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 QY 233 ARGVALALATYRALPROARGASPLAUVALILESERILLESERARGSPASNTHRPROASP 252
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 QY 293 HISSETRPROPROALALARGLEUSERTRTPRHGLINARGGLYGLINVALLEUSERPROSER 312
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 QY 313 GLNPROSERASPROGLYVALLEUGLULEUPROARGVALJLINALGLHISGLUGLYLU 332
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 QY 366 -----GLYALAPHELEUGLYILE 371
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 DB 1503 GGTCTTATGGCCTTGCTGTGCTGTGCTGTGCTCTCTCTTTTTCACAGTGAAGTCTCTC 1562
 QY 390 PROLYSARGHARGHRLNTHRLGUTHRPROARGPROARGPHESEARGHISSETRHILE 409
 DB 1563 AGGAGAAATTCACACC----- 1577
 QY 410 LEUASPTYRILEASNVALYALPROTHRALAGLYPROLEUALAGLINYSARGASNGLINYS 429
 DB 1578 -----CTGAAGTGAAGCTACGAAAGGCAACCATCTTCCCAAG---AACCTGCC 1625
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 DB 1656 TCCACATATTGGCGTTGGGATGATCCCATGCGAGGCTCATCTGTAAGAACACAGGTCACAGAC 1715
 QY 468 RGLN-----ALAPROGLUSERGLINGLUGLULE 480
 DB 1716 CCAGAAAGGACACGCCCTTGGCCACAGTCCGACAGCCCAAAAGATGACGCTTAACCT 1775
 QY 480 WHISTYRALATHLEUASNPHLEUPROGLYVALARGPROARGPROGLUALALARGMETPROLY 500
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RESULT 11
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LOCUS BM906520
DEFINITION AGENCOURT_6620196 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590502
5', mRNA sequence.
ACCESSION BM906520
VERSION BM906520.1 GI:19356899
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1745)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 538.
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49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

BASE COUNT 362 a 493 c 391 g 481 t 18 others
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Alignment Scores:
Pred. No.: 2,31e-44 Length: 1745
Score: 652.00 Matches: 152
Percent Similarity: 53.35% Conservative: 31
Best Local Similarity: 44.31% Mismatches: 81
Query Match: 24.09% Indels: 79
DB: 12 Gaps: 8

US-09-937-636-3 (1-512) x BM906520 (1-1745)

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Db 166 TACAGCTCTCAAGTGCAGAGACAGGTGCGGTCGCGAGGAGGCGCTGTGCATGCTCT 225
QY 41 CysSerPheSerTyrProArgGlnAspTrrThrGlySerThrProAlaTyrGlyTyrTrp 60
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VERSION BM922784.1 GI:19373163
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 995)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

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US-09-937-636-3 (1-512) x BM921873 (1-997)

[illegible]

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IMAGE	30337798 5', mRNA sequence.			
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VERSION	CB992313.1	GI:30268633		
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ORGANISM	Homo sapiens			
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 864)			
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapds@mail.nih.gov			
	Tissue Procurement: Dr. Stefan Hansson			
	cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help			
	and advice from Piero Carninci (RIKEN)			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at:			
	http://image.lnl.gov			
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	size 2.3 kb and normalized to R0F 5. This is a primary			
	library enriched for full-length clones and constructed			
	using the Cap-trapper method (Carninci, in preparation).			
	Library constructed by M. Brownstein (NIH/NHGRI,			
	National Institutes of Health). Note: this is a NIH-MGC			
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ORIGIN				
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Query Match:	22.12%	Indels:	19	
DB:	14	Gaps:	3	
US-09-937-636-3 (1-512) x CB992313 (1-864)				
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Db 214 TCTTCCAAAGCTCTGTGGGTGATGATGCCCTGACCCACAGGCCCAACATCTCCATCCCA 273
QY 152 GluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnThrPalaPheGlu 171
Db 274 GGGACCTGGAGTGTGGCATCCACCAATCTGACCTGCTGTGGCTGTGGTGTGTGAG 333
QY 172 GluCysProProPheSerPheSerThrPheGlyAlaAlaLeuSerSerGlnGlyThrLys 191
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Db 388 CCCAGAGCACCAACAGTCTGTGGGTCTCACAATACACCCAGGCCGCCAGGACACACAGCAC 447
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QY 232 LeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAspAsnThrPro 251
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QY 252 AspProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGluAsn 271
Db 550 -----TTCAAAGGAACACAGCGCAGGCTTCAAAATC 579
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Db 580 CTGCAAAACACCTGCTCCCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 639
QY 292 ThrHisSerSerProAlaArgLeuSerThrPheGlnArgGlyGlnValLeuSerPro 311
Db 640 GCTGACGGCACCCCTGACACACCTGAGCTGTTCCAGGGCTTCCCGGCTTCCGGAACGCC 699
QY 312 SerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnIleGlnGly 331
Db 700 ACCCCCATCTCCAAATACGGGGGTCTGTGAGCTGCTCAAGTAGGCTGTGCAGAGAAAGA 759
QY 332 GluPheThrCysHisAlaArgHisProLeuGlnSerGlnHisVal 346
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Search completed: October 8, 2003, 22:41:04
Job time : 3195 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:04:52 ; Search time 93 Seconds
(without alignments)
2429.980 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLPLLLSLSLGSSQAMDR.....RPARMPKGNADYAEVKR 512

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database :

Issued_Patents_NA:*
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5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	888	32.8	1597	3	US-09-038-832-3
2	888	32.8	2900	3	US-09-038-832-1
3	831.5	30.7	1501	3	US-09-046-736-1
4	573	21.2	1502	3	US-09-046-736-3
5	528.5	19.5	1488	4	US-09-620-312D-407
6	192	7.1	1339	3	US-08-468-856B-3
7	192	7.1	1339	3	US-08-468-856B-3
8	187	6.9	1630	3	US-08-468-856B-2
9	187	6.9	1630	3	US-08-468-856B-2
10	185	6.8	3173	3	US-08-468-856B-1
11	185	6.8	3173	3	US-08-468-856B-1
12	185	6.8	3461	3	US-08-468-856B-6

13	185	6.8	3461	3	US-08-468-859A-6	Sequence 6, Appl
14	177.5	6.6	2166	2	US-08-408-095-30	Sequence 30, Appl
15	172.5	6.4	1348	2	US-09-638-649-6	Sequence 6, Appl
16	167	6.2	1473	2	US-08-602-725-31	Sequence 31, Appl
17	165	6.1	5824	4	US-09-620-312D-72	Sequence 72, Appl
18	159.5	5.9	1024	6	5169835-16	Patent No. 5169835
19	159	5.9	1426	4	US-09-638-649-2	Sequence 2, Appl
20	156	5.8	2458	4	US-09-996-243-502	Sequence 502, App
21	152	5.6	4078	4	US-09-016-434-1120	Sequence 1120, App
22	151.5	5.6	4285	3	US-09-040-774-1	Sequence 1, Appl
23	151.5	5.6	6814	4	US-09-484-970B-66	Sequence 66, Appl
24	147.5	5.5	1718	4	US-09-778-510-5	Sequence 5, Appl
25	145	5.4	1974	4	US-09-423-439-59	Sequence 59, Appl
26	143.5	5.3	1391	4	US-09-638-649-4	Sequence 4, Appl
27	143.5	5.3	1820	4	US-09-778-510-1	Sequence 1, Appl
28	143.5	5.3	2184	4	US-09-484-970B-161	Sequence 161, App
29	143	5.3	2031	1	US-08-217-299-2	Sequence 2, Appl
30	143	5.3	2097	2	US-08-602-725-35	Sequence 35, Appl
31	143	5.3	2220	1	US-08-389-459A-16	Sequence 16, Appl
32	143	5.3	2220	3	US-08-987-867A-16	Sequence 16, Appl
33	143	5.3	2349	2	US-08-184-009-145	Sequence 145, App
34	143	5.3	2349	2	US-08-458-356-145	Sequence 145, App
35	143	5.3	2349	3	US-08-460-736-145	Sequence 145, App
36	143	5.3	2349	4	US-09-535-370-145	Sequence 145, App
37	143	5.3	2434	2	US-08-184-009-144	Sequence 144, App
38	143	5.3	2434	2	US-08-458-356-144	Sequence 144, App
39	143	5.3	2434	3	US-08-460-736-144	Sequence 144, App
40	143	5.3	2434	4	US-09-535-370-144	Sequence 144, App
41	142.5	5.3	1693	2	US-08-487-113D-118	Sequence 118, App
42	142.5	5.3	1693	2	US-08-720-420A-118	Sequence 118, App
43	140	5.2	1273	4	US-09-778-510-3	Sequence 3, Appl
44	138.5	5.1	1542	4	US-09-205-258-123	Sequence 123, App
45	138	5.1	1693	6	5169835-3	Patent No. 5169835

ALIGNMENTS

RESULT 1
US-09-038-832-3
; Sequence 3, Application US/09038832
; Patent No. 6146845
; GENERAL INFORMATION:
; APPLICANT: KIRKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Stalodhesin Family Member-2
; NUMBER OF INVENTION: (SAF-2)
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038.832
; FILING DATE: 11-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,886
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701

Db 957 -----GCAGCGACGTGGAGACATAGCATGAAG----- 986
 QY 428 GlnYsAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu 447
 Db 987 -----GATGCAAAACCCATCAGG 1004
 QY 448 SerLysLysAsnGlnLysGlnTyrGlnLeuProSerPheProGluProLysSer 467
 Db 1005 GGCCTCAGCCTCTCAGTACCTGACTGATCTCTGGCAGATGATACCCCGACACCAT 1064
 QY 468 ThrGlnAlaProGluSerGlnGlnSerGlnGlnGlnLeuHisTyrAlaThrLeuAsnPhe 487
 Db 1065 GCGCTGCTGCCACTCTCTCAGGAGGAGAAAGATCCAGTATGACCCCTCAGCTTT 1124
 QY 488 ProGlyValArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAla 507
 Db 1125 CATAGGGGGAGCCCTCAG---GACCTATCAGGTCAAGAACCCACCAACATGAGTACTCA 1181
 QY 508 GluValLys 510
 Db 1182 GAGATCAAG 1190

RESULT 5

US-09-620-312D-407
 Sequence 407, Application US/09620312D
 Patent No. 6569662
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John, Tillinghast
 APPLICANT: Dimanac, Radoje T.
 TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/09/620, 312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552, 317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488, 725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: Pf-Fl.genes Version 1.0
 SEQ ID NO 407
 LENGTH: 1488
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (146)..(931)
 US-09-620-312D-407

Alignment Scores:

Pred. No.: 1,8e-41 Length: 1488
 Score: 528.50 Matches: 145
 Percent Similarity: 47.42% Conservative: 66
 Best Local Similarity: 32.58% Mismatches: 139
 Query Match: 19.53% Indels: 98
 DB: 4 Gaps: 12

US-09-937-636-3 (1-512) x US-09-620-312D-407 (1-1488)

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 Db 722 CCCGAGCTGTGTGACGACGAGAGAACCATCCAGCTCATGCTCTCTGGAATCAGGA 781
 QY 237 ---AlaProArgAspLeuValIleSerIleSerArgAspAsnThrProAspPro----- 253
 Db 782 ACCGTGAGAGAGGGGTGTTGTTTGGCCGTGGGGT-AGTGGCTGTGAAGATCCGTCTT 840
 QY 254 -----ProGluAsn----- 256
 Db 841 CTGCTTTGGCTCATCTCTCAGTTTCCACAAAGAAAGCGGTGAGCGAGTGAAGT 900
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 QY 271 AsnLeuGlyAsnGlyThrSerLeuProVal----- 280
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 QY 281 ---LeuGlnGlyGlnSerLeuCysLeu-----ValCysValThrHis 293
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Oy 353 sTyGfAlaGlyGlyleuIleSerThrAlaPheSerAsnGlyAlaPheleuGlyIleGlyTf 373
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Oy 373 ethAlaIleu-----PheleuGlyleuAl 382
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Oy 382 AleuIleIleMet 386
Db 1284 TTGTATGATATTA 1296

RESULT 6
US-08-468-8568-3
Sequence 3, Application US/08468856B
Patent No. 6013772
GENERAL INFORMATION:
APPLICANT: Barnett, Thomas; Eling, James; Kamarch, Michael;
APPLICANT: Kretschmer, Axel
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer & Woods
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 2.0 MB storage
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WordPerfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,856B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/274,107
FILING DATE: 21-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,678
FILING DATE: 16-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/060,031
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/016,683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896,361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: M01 242.10-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700

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TELEFEK: (914) 332-1844	INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:	
LENGTH: 1339 nucleotides	
TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
US-08-468-856B-3	
Alignment Scores:	
Pred. No.:	5,45e-09
Score:	192.00
Percent Similarity:	34.99%
Best Local Similarity:	22.10%
Query Match:	7.10%
DB:	3
Length:	1339
Matches:	120
Conservative:	70
Mismatches:	170
Indels:	183
Gaps:	27
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25 ValGlnGlnSerValMetValProGluGlyLeuGlyIleSerValPro-----	40
163 CCCAGCACCTGCCAGCTCACTACTAGTAATCCATGCAATGTTGACGAGGGAGAG	222
41 -----CysSerPheSerTyrrProArgGlnAspTrpGlnGlySerThrProAlaTyrr	57
223 GTTCTTCTCTCTTCTCCACAAATCTGCCCCACGAA-----CTTTT	261
58 GlyTyrr--TrpPheLysAlaValThrGluThrLysGlyAlaProValAlaThrAsn	76
262 GCGTCAACAGCTGACAAAGG-----GAAGAGTGATGCG-----	297
77 HisGlnSerArgGluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro	96
298 -----AACCGTAAATTTAGAGATATGCAATAGGAACCTCAACAGCTACCCAGGCCC	351
97 AlaLysGly-----AsnGlySerLeuValIleArgAspAlaGln	109
352 GCAACAGCCGCTGGAAGACAAATATACCCCAATGCATCCGTCGATGCCAACAAGCTCAC	411
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412 CAGAATGACACAGAGATTCTACACCTACACAGTC-----ATTAAGTCAGAT	456
130 PheMetAsnAspGlyPhePheLeuLeuValThrAlaLeuThrGlnLysProAspValTyrr	149
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150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla	169
495 -----	495
170 PheGluGlnCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly	189
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190 ThrLysProThrThrThrSerHisPheSerValIleUserSerPheThrProArgProGlnAspHis	209
532 TCCAAACCTCTGTGAGAGACAAGATGCTGTG---GCCCTCACCTGTGAACCTGAAACGTCAG	588
210 AspTrpAspLeuThrCysHisValAspPheSerArgLysGlyValSerIleArgGlnArgThr	229
589 GACACAAACCTACTGTGTGGATAAACAATCAGACCTCCGGGTACGTCCTC-----	639
230 ValArgLeuArgValAlaTyrrAlaProArgAspLeu---ValIleSerIleSerArgAsp	248
640 ---AGGCTGACGCTGTCCAATGGCAACAGACCTCACCTACATCAGTACGTCACAAAGAT	696
249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr---	267

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Db 754 CCACTGACACTTGAATGTACCTATATGGCCGAGACACCCACCACTATTTCCCTTCAGACACC 813
Qy 283 -----GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAla 298
Db 814 TATTACCGTCCAGGGGCAACCTCAGGCTCTCTGATATGACGAGCTTACACCACTGCA 873
Qy 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
Db 874 CAGTACTCTGGCTTATCAATGAAACATTCACGCAAAAGCACACAGAG-----921
Qy 319 ValLeuGluLeuProArgValGlnValGlnHisGlnGlyGluPheThrCysHisAlaArg 338
Db 922 ---CTTTTATTCCTATACATCAGCTGTGATATATAGTGATCTTATACCTGCACGCCAT 978
Qy 339 HisProLeu---GlySerGlnHisValSerLeuSerValHisTyrLeuLysGly 357
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Qy 358 Leu---IleSerThrAlaPheSerAsnGlyAlaPheLeuGly-----IleGlyTleThr 374
Db 1039 CTACCACAGAAATAATGGCTCTCTCACCTGGGCGCATTTGCTGCAATGTGATGAGTAGTG 1098
Qy 375 AlaLeuLeu---PheLeuCysLeuAlaLeuIle-IleMetLysIleLeuProLysArgAr 393
Db 1099 GCCCTGGTCTCTGATACGACATGACCCCTGGCATGTTTCTGCAT-----1144
Qy 393 GThGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrI1 413
Db 1145 -----TCGGGAAGACCGGAGCTCAGAGCACCTCCAT-----1177
Qy 413 eAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAs 433
Db 1177 -----1177
Qy 433 nSerProArgThrProLeuProProGlyAlaProSerProGluSerLysAsnGlnLys 453
Db 1178 -----GACCCACCTAACAGATGAT-----1198
Qy 453 sLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSe 473
Db 1198 -----1198
Qy 473 rGlnGlnSerGlnGlnGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgPro-- 492
Db 1199 -----GAAGTACTTATTTTACCTTGAACCTTGAAGCCGACCAACCCAC 1242
Qy 493 -ArgProGluAlaArgMetProLys-----GlyThrGlnAlaAspTyrAlaGluVally 510
Db 1243 ACAACCAACTTACAGCTCCCATGCCATACAGCCACAGCAAAATATTTATTCAGAAAGTAA 1302
Qy 510 sPheGln 512
Db 1303 AAAGCAG 1309

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; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468, 859A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027, 974
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/760, 031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274, 107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207, 678
; FILING DATE: 16-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/060, 031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016, 683
; FILING DATE: 19-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/896, 361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1339 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-468-859A-3
; Alignment Scores:
; Pred. No.: 5.45e-09 Length: 1339
; Score: 192.00 Matches: 120
; Percent Similarity: 34.99% Conservative: 70
; Best Local Similarity: 22.10% Mismatches: 170
; Query Match: 7.10% Indels: 183
; Gaps: 27
; US-09-937-636-3 (1-512) x US-08-468-859A-3 (1-1339)
Qy 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrIleArg 24
Db 127 CTGCTCACAGCCTTACTTCTTA-----ACCTTCTGGAACCGG 162
Qy 25 ValGlnGlnSerValMetValProGluGlyLeuGlyLysIleSerValPro-----40
Db 163 CCCACCACTGCCGACGCTACACTGAAATGCAATGCCATTCATGTCGAGAGGAGAGAG 222
Qy 41 -----CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr 57
Db 223 GTTCTCTCTCTTGTGCACAAATCTGCCCCAGCA-----CTTTT 261
Qy 58 GlyTyr---TrpPheLysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsn 76
Db 262 GGTACAGCTGTGTACAAAGG-----GAAAGAGTGGATGGC-----297

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OY	77	HisGlnSerArgGluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlnLysPro	96
Db	298	-----AACGCTCAAAATTGTAGATATGCAATAGCAACTCAACCAAGCTACCCAGGGCC	351
OY	97	AlaLysGly-----AsnCysSerLeuValIleArgAspAlaGln	109
Db	352	GCAAAACAGCGGTCGAGAACAAATATATACCCCAATGATGATCCCTGCTATATCCAGAACCTCAC	411
OY	110	MetGlnAspGlnSerGlnTyrPhePheArgValGlnArgGlySerTyrValArgTyrAsn	129
Db	412	CAGAAATGACACAGAGATTCTACACCCCTACAGTGC-----ATAAAGTCAGAT	456
OY	130	PheMetAsnArgGlyPhePheLeuLysValIleThrAlaLeuThrGlnLysProAspValTyr	149
Db	457	CTTGTGAATTGAA-----GAAGCAACTGACATTCCTCATATATAC	495
OY	150	IleProGlnThrLeuGlnProGlyLysProValIleThrValIleCysValPheAsnThrAla	169
Db	495	-----	495
OY	170	PheGlnGluCysProProProSerPheSerThrThrGlnAlaAlaLeuSerSerGlnGly	189
Db	496	---CCGAGAGCTGCCCAACGCTCC-----ATCTCCAGCAACAC	531
OY	190	ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis	209
Db	532	TCCAACTCGTTGGAGGACAGACAGATGCTGTG---GCCCTTACCTGTGAACCTGACATCAG	588
OY	210	AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr	229
Db	589	GACACACACCTACCTGTGGATTAACAATACAGACCTCCCGGAGTACGCC-----	639
OY	230	ValArgLeuArgValAlaTyrAlaProArgAspLeu---ValIleSerIleSerArgAsp	248
Db	640	---AGGCTGACAGCTGTCCATGCGCAACGACACCTCTACTGATCAGTGTGCACAGGAT	696
OY	249	AsnThrProAspProProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThr---	267
Db	697	GACACAGACCCCTATGACTGTGAATATGACGAACCCAGTGAAGT---GCCAACGCCAGTGCAC	753
OY	268	---ValLeuGlnAsnLeuGlyAsnGlnThrSerLeuProValIleGlu---	282
Db	754	CCAGTCACTTGAAATGTACCTATATGCCCCGGACACCCCACTTCTCCCTTCAGACAC	813
OY	283	-----GlyGlnSerLeuCysLysValCysValIleThrHisSerSerProAla	298
Db	814	TATTACCTGCACAGGGGCAACCTGACGCTCTGCTGTGACGCTCTTAACCCACTGCA	873
OY	299	ArgLeuSerThrThrGlnArgGlyLysValLeuSerProSerGlnProSerAspProGly	318
Db	874	CAGTACTCTGGCTTATATCAATGACAATTCACGAAACACCAACAG-----	921
OY	319	ValLeuGlnLeuProArgValGlnValGlnAsnGlnGlyLysPheThrCysHisAlaArg	338
Db	922	---CTCTTATACCTTACATCAGCTGTGAATAATAGTGGATCTTAATCCGCACGCCAAT	978
OY	339	HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTyrLysGly	357
Db	979	AACTCAGTCACTGGCTGCACAGACGACACACGTCAGACAGATCATGTCATGATTAATGCT	1038
OY	358	Leu---IleSerThrAlaPheSerAsnGlyAlaPheLeuGly-----IleGlyIleThr	374
Db	1039	CTACCACAAAGAAATGGCTCTCTACCTGGGGCCATTCGCTCATTTGTGTGAGTATG	1098
OY	375	AlaLeuLeu---PheLeuCysLeuAlaLeuIle-IleMetLysIleLeuProLysArgAr	393
Db	1099	GCCCTGGTGGCTGTGATAGCAGTACCTTGGCATGTCTTTCTGCATTT-----	1144
OY	393	GThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIle	413
Db	1145	-----TCGGGAGACCGGCGACGTTCAGGACCATCTCAAT-----	1177
OY	413	AsnAsnValProThrAlaGlyLysProLeuAlaGlnLysArgAsnGlnLysAlaThrProAs	433

Db	1177	-----	1177
Qy	433	nSerProArgThrProLeuProProGlyAlaProSerProGluSerLysAsnGlnIly	453
Db	1178	-----	1198
Qy	453	slyGcIntYrcInteuproSerPheProGluProLysSerSerThrGlnAlaProGluSe	473
Db	1198	-----	1198
Qy	473	rgInGluSerGlnGlnGluLeuHisTYrAlaThrLeuAsnPheProGlyValArgPro--	492
Db	1199	-----	1242
Qy	493	ArgProGluAlaArgMetProLys-----GlyThrGlnAlaAspTYrAlaGluValIly	510
Db	1243	ACAACCAACTTCAGCCCTCCCATCCCTAACAGCCACAGCAATTAATTATTCAGAAAGTMAA	1302
Qy	510	sPheGln 512	
Db	1303	AAAGCAG 1309	
RESULT 8			
US-08-468-8568-2			
Sequence 2, Application US/084688568			
Patent No. 6013772			
GENERAL INFORMATION:			
APPLICANT: Barrett, Thomas; Eling, James; Kamarch, Michael;			
APPLICANT: Kretschmer, Axel			
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE			
TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY			
NUMBER OF SEQUENCES: 14			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Sprung Horn Kramer & Woods			
STREET: 660 White Plains Road			
CITY: Tarrytown			
STATE: New York			
COUNTRY: USA			
ZIP: 10591-5144			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage			
COMPUTER: APPLE MACINTOSH 6500			
OPERATING SYSTEM: SYSTEM 7.5			
SOFTWARE: Wordperfect 3.5			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/468,8568			
FILING DATE: 06-JUN-1995			
CLASSIFICATION: 424			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/027,974			
FILING DATE: 08-MAR-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/760,031			
FILING DATE: 13-SEP-1991			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/274,107			
FILING DATE: 21-NOV-1988			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/207,678			
FILING DATE: 16-JUN-1988			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/060,031			
FILING DATE: 19-JUN-1987			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/016,683			
FILING DATE: 19-FEB-1987			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 06/896,361			
FILING DATE: 13-AUG-1986			
ATTORNEY/AGENT INFORMATION:			
NAME: Kuit G. Briscoe			
REGISTRATION NUMBER: 33,141			

RESULT 8
US-08-468-856B-2
Sequence 2, Application US/08468856B
Patent No. 6013772
GENERAL INFORMATION:
APPLICANT: Barnett, Thomas; Elting, James; Kameark, Michael
APPLICANT: Kretschmer, Axel
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spring Horn Kramer & Woods
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 2.0 Mb storage
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: Wordperfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,856B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/274,107
FILING DATE: 21-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,678
FILING DATE: 16-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/060,031
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/016,683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896,361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: Kuit G. Britscoe
REGISTRATION NUMBER: 33,141

REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-856B-2

Alignment Scores:
Pred. No.: 2,28e-08 Length: 1630
Score: 187.00 Matches: 125
Percent Similarity: 36.25% Conservative: 86
Best Local Similarity: 21.48% Mismatches: 206
Query Match: 6.91% Indels: 165
Gaps: 28
DB:

US-09-937-636-3 (1-512) x US-08-468-856B-2 (1-1630)

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QY 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrPLeuArg 24
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Db CTGCTCACAGCCTCACTTCTA-----ACCTTCTGGAACCCG 162

QY 25 ValGlnGluSerValMetValProGluGlyLeuGlyIleSerValPro-----40
   :|||:|||||
Db 163 CCCACCACTGCCAGCTACTACTGAAATCCATTCATCAATGTTGCCAGACGGAGAG 222

QY 41 -----CysSerPheSerTyProArgGlnAspTrpThrGlySerThrProAlaTy 57
   :|||:|||||
Db 223 GTTCTTCCTGCTGTCACAAATCTGCCACAGCA-----CTTTT 261

QY 58 GlyIyr---TrpPheIysAlaValThrGluThrThrIlysglyAlaProValAlaThrAsn 76
   ||||| :|||:|||||
Db 262 GGTACACAGCTGTGTCACAAAGG-----GAAAGAGTGATGTC-----297

QY 77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
   :|||:|||||
Db 298 -----AACCTCAATTGTAGATATGCCAATAGCAATCAACAAGCTACCCGAGGCC 351

QY 97 AlaIysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
   ||| :|||:|||||
Db 352 GCAAAACAGCGTGCAGAGACAATATACCCCAATGATCCCTGTGATCCAGACGTCACC 411

QY 110 MetGlnAspGluSerGlnTyPhePheArgValGluArgGlySerTyValArgTyAsn 129
   ||| :|||:|||||
Db 412 CAGAAATGACACAGAAATCTACACCCCTACAGTC-----ATAAAGTCAGAT 456

QY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTy 149
   :|||:|||||
Db 457 CTGTGATGTA-----GAGCAACTGGACAGATTCATCATGTATAC 495

QY 150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla 169
   :|||:|||||
Db 495 -----495

QY 170 PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189
   ||||| :|||:|||||
Db 496 ---CCGAGCTGCCCAAGCCTCC-----ATCTCAGCAGACAC 531

QY 190 ThrIysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209
   :||| :|||:|||||
Db 532 TTCAAACCTGTGGAGGACAAAGATGCTGTG---GCCTCACCTGTGAACGACGCTAG 588

QY 210 AspThrAspLeuThrCysHisValAspPheSerArgIlysglyValSerAlaGlnArgThr 229
   ||||| :|||:|||||
Db 589 GACACAACTCACTGCTGGTGAATAACATCAGAGCCCTCCGTCAGATCCC-----639

QY 230 ValArgLeuArgValAlaTyAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
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Db 640 ---AGGTCGAGCTGTCCAAATGGAACAGGACCTCACTACTGATGTCACAAAGGAT 696
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QY 249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr---267
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Db 697 GACACAGGACCCCTTGTAGTGTGAATATACAGAACCACTGAT---GGCAACCGAGTGAC 753

QY 268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu-----282
   ||| :|||:|||||
Db 754 CCAGTCACCTGTAATGATCAACTATAGGCCCGGACACCCACCATTTCCCTTCAGACACC 813

QY 283 -----GlyGlnSerLeuCysLeuValLysValThrHisSerSerProAla 298
   ||| :|||:|||||
Db 814 TATTACCGTCCAGGGGGAACCTCAGCTCTCTGCTATGACGCTTAAACCACTGCA 873

QY 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
   :|||:|||||
Db 874 CAGTACTCTGCTGCTTATCATATGAAATCCAGCAAGACACAAAGAG-----921

QY 319 ValLeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArg 338
   ||| :|||:|||||
Db 922 ---CTCTTATCCCTTAACATCAGCTGTAATATAGTGAATGATGATCTTACCTGCGCCCAAT 978

QY 339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTyIlysgly 357
   :|||:|||||
Db 979 AACTCAGTCACTGCTGCCAAGACCAAGACCAAGTC-----AAGACG 1017

QY 358 LeuIleSerThrAlaPheSer-----364
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Db 1018 ATCATAGTCACTGAGCTAAGTCCAGTAGTACCAAGCCCAATCAAAAGCCAGCAAGACC 1077

QY 365 -----AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAla 382
   ||| :|||:|||||
Db 1078 ACAGTCAAGAGAGATTAAGAGACTGTGTGAACCTGAC-----TGCTCCACA 1122

QY 383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrPro 399
   ||| :|||:|||||
Db 1123 AATGACACTGGAATCTCATCTGCTGTGTTCTTCAAAAACGAGATCCCTGCTCGAG 1182

QY 400 ArgProArgPheSerArgHisSerThrIleLeuAspTyIleAsnValValPro---ThrAl 419
   ||| :|||:|||||
Db 1183 AGATGAAGAGCTGCTCCAGGAGCAACACCACTC-----ACATTAACCTGTGCAAG 1233

QY 419 ArgProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLe 439
   ||| :|||:|||||
Db 1234 AGGAGAGATGTGGAGGATATGTTGTGAGGCTTTCACCACTCACTAAGAACCAAGC 1293

QY 439 uProProGlyAlaProSerProGluSerLysAsnGlnLysLysGlnTyArgIn-----457
   ||| :|||:|||||
Db 1294 GACCCCATCATGCTGAACGTAACTATATGCTCTACACAGAAATGGCTCTCACT 1353

QY 458 -----LeuProSerPhePro-----462
   ||| :|||:|||||
Db 1354 GGGGCCATGCTGCGCATTTGTGATGTAGTATGAGTGGCCCTGCTGTGATAGCAGTAGCC 1413

QY 463 -----GluProLysSerSerThrGlnAlaProGluSerGln 474
   ||| :|||:|||||
Db 1414 CTGGCAATGTTTTCGCAATTTTGGGAAGACCGGACGCTCAGACCACTCCATATGACCAACC 1473

QY 474 nGluSerGlnGluLeuHisTyArgAlaThrLeuAsnPheProGlyValAlaArgPro---Ar 493
   :|||:|||||
Db 1474 TAACAAGATGAATGATATGATTAATTCACCTGTAACCTTGAAGCCAGCAACACACACA 1533

QY 493 gProGluAlaArgMetProLys-----GlyThrGlnAlaAspTyArgIlysglyValIlyspH 511
   :||| :|||:|||||
Db 1534 ACCAAGTCAAGCTCCCATCCCATCCATACAGCCACAGAAATATTAATTCAGAAATGAAA 1593

QY 511 eGln 512
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Db 1594 GCAG 1597
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RESULT 9
US-08-468-859A-2
; Sequence 2, Application US/08468859A
; Patent No. 6022958

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GENERAL INFORMATION:
APPLICANT: Barnett, Thomas; Eiting, James; Kamarch, Michael;
APPLICANT: Kreschmer, Axel
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
NUMBER OF INVENTION: CARCINOMEMBRYONIC ANTIGEN FAMILY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer & Woods
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: Wordperfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468, 859A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027, 974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760, 031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/274, 107
FILING DATE: 21-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207, 678
FILING DATE: 16-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/060, 031
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/016, 683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896, 361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-859A-2

Alignment Scores:
Pred. No.: 2,28e-08 Length: 1630
Score: 187.00 Matches: 125
Percent Similarity: 36.25% Conservative: 86
Best Local Similarity: 21.48% Mismatches: 206
Query Match: 6.91% Indels: 165
DB: 3 Gaps: 28

US-09-937-636-3 (1-512) x US-08-468-859A-2 (1-1630)
OY 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAlaSpGlyAlaArgPheTrpIleArg 24
DB 127 CTGCTCACAGCCTCACTCTTA-----ACCTTCGGAACCCG 162
OY 25 ValGlnGluSerValMetValProGlnGluGlyLeuGlySileSerValPro----- 40

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DB 163 CCACACACGCCACAGCTACTGATGATGCAATGCCATTCGAAATGTCACAGGGGAGAGAG 222
OY 41 -----CysSerPheSerTrpProArgGlnAspTrpThrGlySerThrProAlaTrp 57
DB 223 GTTCTTCCTTCCTTGCACCAATCTGCCCCAGCAA-----CTTTT 261
OY 58 GLTYR-----TriPheLysAlaValAlaThrGluTrpThrLysGlyAlaProValAlaTrpAsn 76
DB 262 GGTACAGCTGTGTACAAAGG-----GAAGAGTGGATGC----- 297
OY 77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
DB 298 -----AACCGTCAATGTAGATATGCAATAGAACATCAACAAGCTACCCAGGCC 351
OY 97 AlaLysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
DB 352 GCAACACGGCTGCAGAGACAATATACCCCAATGCATCCCTGCTGCAGAACGTCAC 411
OY 110 MetGlnAspGluSerGlnTrpPhePheArgValGluArgGlySerTrpValaArgTrpAsn 129
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OY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTrp 149
DB 457 CTTGTGAATGAA-----GAAGCAACTGGACAGTTCATGTATAC 495
OY 150 IleProGluThrLeuGluProGlnProValThrValIleCysValPheAsnTrpAla 169
DB 495 ----- 495
OY 170 PheGluGluCysProProSerPheSerTrpThrGlyAlaAlaLeuSerGlnGly 189
DB 496 ---CCGAGCTGCGCAAGCCTCC-----ATCTCCAGCAACAC 531
OY 190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209
DB 532 TCCAAACCCGTGGAGACACAAGATGCTGTG---GCCTTACCTGACCTGAGACTGAC 588
OY 210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229
DB 589 GACACAACTTACCCTGTGTGATTAACAATCAAGAGCTCCGCTGCC----- 639
OY 230 ValArgLeuArgValAlaThrAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
DB 640 ---AGCTGACAGCTGCAATGCAACAGAGACCTCACTACTGCTACACAAAGGAT 696
OY 249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267
DB 697 GACACAGAGACCTATGAGTGTGAATATACAGAACCCAGTGTAGT---CGAAGCCGAGTAC 753
OY 268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu----- 282
DB 754 CCAGTCACCTTGAATGCAATATGAGCCGCGACACCCCAACCATTTCCCTTCACAGAC 813
OY 283 -----GlyGlnSerLeuGlyValGlyValThrHisSerSerProProAla 298
DB 814 TATTACCGTCCAGGGGCAAACTCAGCCTCTCTCTATAGACAGCTTAACCACTGGA 873
OY 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerArgProGly 318
DB 874 CAGTACTCTGCTGTATGCAATGCAATTCACACAAAGACACACAGAG----- 921
OY 319 ValLeuGluLeuProArgValGlnValGluHisGlyGlyGluPheThrCysHisAlaArg 338
DB 922 ---CTCTTATATCCCTTGAATGATATAGTATAGTCCATATACCTGCACGCCAAT 978
OY 339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTrpLysGly 357
DB 979 AACTCAGTCACTGCTGCAACAGAGACCAAGTCACTGCACTGCACTGCACTGCACTG 1017
OY 358 LeuIleSerThrAlaPheSer-----AAGAGC 364

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Db 1018 ATCATAGTCACTGAGTAACTAGTCCAGTAGTACCAAGCCCAATCAATCAAGCAGCAAGACC 1077
QY 365 -----AsnGLyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuGlyLeuAla 382
Db 1078 AAGAGTCACAGAGATRAAGACTCTGTGAACCTGACC-----TGCTCCACA 1122
QY 383 Leu-----IleIleMetIleLeuProIlePheArgArgThrGlnThrGlnThrPro 399
Db 1123 AATGACACTGCAATCTCCATCGGTGGTCTTCAAAAACCAAGCTCCCGCTCCGGAG 1182
QY 400 ArgProArgPheSerThrHisSerThrIleLeuAspTyrIleAsnValAlaPro--ThrAl 419
Db 1183 AGGATGAAGCTGTCCAGGCAACACCCCTC-----AGCATTAACCTGTCTCAG 1233
QY 419 aGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProle 439
Db 1234 AGGAGAGATGCTGGGAGACGATTTGGTGAGGCTTCAACCAATCAATCAAGCAACCAAGC 1293
QY 439 uProGlnLysAlaProSerProGlnSerLysAsnGlnLysGlnTyrGln----- 457
Db 1294 GACCCATCACTGCTGAAGCTAACTAATGCTTACCAAGAAATGGCCTCAGCT 1353
QY 458 -----LeuProSerPhePro----- 462
Db 1354 GGGCCATTGCTGCATTGTGATGAGTACGTGGCCGTGCTGTGATAGCAGTACCC 1413
QY 463 -----GluProLysSerSerThrGlnAlaProGlnSerGln 474
Db 1414 CTGGCATGTTTTCGATTTGGGGAAGCGGAGCTGAGCAGCAGCAGTCAATGCC 1473
QY 474 nGluSerGlnGlnGlnLeuHisTyrAlaThrLeuAsnPheProGlnValAlaPro--Ar 493
Db 1474 TAACAAGATGATAGTAACTTATCTTACCTGATGATGATGATGATGATGATGATGAT 1533
QY 493 gProGlnAlaArgMetProLys-----GlyThrGlnAlaAspTyrIleValLysPhe 511
Db 1534 ACCAACTCAAGCCCTCCCATCCCTACAGCCAGCAAGAAATATTATTTCAGAAATAAAA 1593
QY 511 eGln 512
Db 1594 GCAG 1597

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RESULT 10
US-08-468-856B-1
Sequence 1, Application US/08468856B
Patent No. 6013772
GENERAL INFORMATION:
APPLICANT: Barnett, Thomas; Eiting, James; Kamarch, Michael;
APPLICANT: Kretschmer, Axel
TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer & Woods
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WordPerfect 3.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,856B
CLASSIFICATION: 424
FILING DATE: 06-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031

```

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FILING DATE: 13-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/274,107
FILING DATE: 21-NOV-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/207,678
FILING DATE: 16-JUN-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/060,031
FILING DATE: 19-JUN-1987
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/016,683
FILING DATE: 19-FEB-1987
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 06/896,361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3173 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-856B-1
Alignment Scores:
Pred. No.: 1.04e-07
Score: 185.00
Percent Similarity: 35.04%
Best Local Similarity: 21.90%
Query Match: 6.84%
DB: 3
Caps: 28
US-09-937-636-3 (1-512) x US-08-468-856B-1 (1-3173)
QY 5 LeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrIleArg 24
Db 127 CTGCTCAGCCCTCAGCTCTA-----ACCTCTGGAACCG 162
QY 25 ValGlnGluSerValMetValProGlnGlyLeuGlyIleSerValPro----- 40
Db 163 CCCACACACTGCCCCAGCTCACTACTGAATCCATCCATCAATGTCAGAGGGAAGAG 222
QY 41 -----CysSerPheSerTyrProArgGlnAspTyrThrGlySerThrProAlaTyr 57
Db 223 GTTCTTCCTCCTGTCACAAATGCCCCAGCA-----CTTTT 261
QY 58 GlyTyr---TyrPheLysAlaValIleGlnThrThrLysGlyAlaProValAlaThrAsn 76
Db 262 GGCTACAGCTGTACAAAGG-----GAAGAGTGATGGC----- 297
QY 77 HisGlnSerArgGlnValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
Db 298 -----AACCGTCAATTTAGATATGCAATRAAGACTCAACACCAAGGAGGCCC 351
QY 97 AlaLysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
Db 352 GCAAACAGCGGTGAGAGACAATATACCCCAATGATCCCTGCTGATCCAGAACGTCAC 411
QY 110 MetGlnAspGlnSerGlnTyrPhePheArgValGlnArgGlySerTyrValArgTyrAsn 129
Db 412 CAGATGACACAGAAATTTCAACCTTACAGTC-----ATAAGTCAGAT 456
QY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149
Db 457 CTGTGCAATGAA-----GAAGCACTGAGACAGTTCCATGTATAC 495

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QY 150 lIeProGluThrLeuGluProGluGlnProValThrValIleCysValPheAsnTrpAla 169
DB 495 -----
QY 170 PheGluGluCysProProSerPheSerTrpThrGlyAlaAlaLeuSerGlnGly 189
DB 496 ---CCGGAGCTGCGCCCAAGCCCTCC-----ATCTCCACCAACAC 531
QY 190 ThrLysProThrThrSerHisPheSerAlaLeuSerPheThrProArgProGlnAspHis 209
DB 532 TCCAACCTCTGTGGAGACAAGCATGCTGTGGCTCC---ACCTGTGAACCTGTGAGCTCAG 588
QY 210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229
DB 589 GACACAACTACTCTGTGGTGGATTAACAATCAAGAGCTCCCGGTACGTCC----- 639
QY 230 ValArgLeuArgValAlaTrpAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
DB 640 ---AGCTGCAGCTGTCCAAATGCGCAACAGCAGCCCTCACTCACTCACTGTCACAGAGAAAT 696
QY 249 AsnThr---ProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267
DB 697 GACACAGACCCCTATAGTGTGAAATACAGAACCCAGTGAAGTCCGAACCTCACTGACCCCA 756
QY 268 ValLeuGluAsnLeuGlnGlyThrSerLeuProValLeuGlu----- 282
DB 757 GTACACTTGATTCACCTATGCGCGGACACCCCACTTCCCTTCAGACACTAT 816
QY 283 -----GlyGlnSerLeuCysLeuValCysValThrHisSerSerProAlaArg 299
DB 817 TACCGTCAAGGCGCAAAACCTCAGCCTCTCTGCTATGACAGCCTTAACCCAGCTGCAGAG 876
QY 300 LeuSerTrpThrGlnArgGlnValLeuSerProSerGlnProSerArgProGlyVal 319
DB 877 TACTCTGCTGTTATCAATGGACATTCACCAAGAACCAACAG----- 921
QY 320 LeuGluLeuProArgValGlnValGlnHisGluGlnPheThrCysHisAlaArgHis 339
DB 922 CTCTTTATCCCTAACATCACTGATGAAATAGTGAAATCCATACCTGCGCAGCCCAATAC 981
QY 340 ProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTrpLysGlyLeu 358
DB 982 TCAGTCACTGGCTGCAACAGCAGCAGCATCAAGACATCAATGCTGATTAATGCTCTA 1041
QY 359 ---IleSerThrAlaPheSerAsnGlyAlaPheLeuGly-----IleGlyIleThrAla 375
DB 1042 CCACAAGAAAATGGCTCTCACCCTGGGCGCATTTCTGCTGATTTGGAGTAGTGCC 1101
QY 376 LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeu----- 389
DB 1102 CTGCTTGCTCTG---ATAGCAGTAGCCCTGCGCATGTTTCTGCATTTCCGGAGACCGGC 1158
QY 390 -----ProLysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSer 407
DB 1159 AGGCAAGCGCAGCAGCGGTATCTACAGAG---CACAAACCTCAGTCTCAACACACACT 1215
QY 408 ThrIleLeuAspTrpIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsn 427
DB 1216 CAG-----GACCACATCCAAAT----- 1230
QY 428 GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu 447
DB 1231 -----GACCCACCT 1239
QY 448 SerLysLysAsnGlnLysLysGlnTrpGlnLeuProSerPheProGluProLysSerSer 467
DB 1240 AACAAGATGAAT----- 1251
QY 468 ThrGlnAlaProGluSerGlnGluSerGlnGluLeuHisTrpAlaThrLeuAsnPhe 487
DB 1252 -----GAACTTACTTATTTCTACCTGAACTTT 1278
QY 488 ProGlyValAlaArgPro---ArgProGluAlaArgMetProLys-----GlyThrGlnAla 504

```

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DB 1279 GAAGCCAGCAACCCACACACCACTTCAGCTCCCATCCCTAACAGCCACAGAAATA 1338
QY 505 AspTrpAlaGluValLysPheGln 512
DB 1339 ATTATTCAGAAAGTAAAAAGCAG 1362

RESULT 11
US-08-468-859A-1
; Sequence 1, Application US/08468859A
; Patent No. 6022958
; GENERAL INFORMATION:
; APPLICANT: Barnet, Thomas; Eiting, James; Kowarck, Michael;
; APPLICANT: Krieschmer, Axel
; TITLE OF INVENTION: CDNA CODING FOR MEMBERS OF THE
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sprung Horn Kramer & Woods
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,859A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,974
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/760,031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274,107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207,678
; FILING DATE: 16-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/060,031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016,683
; FILING DATE: 19-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/896,361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3173 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-468-859A-1

Alignment Scores:
Pred. No.: 1,04e-07 Length: 3173
Score: 185.00 Matches: 120
Percent Similarity: 35.04% Conservative: 72

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: FILING DATE: 08-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/760,031
: FILING DATE: 13-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/274,107
: FILING DATE: 21-NOV-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/207,678
: FILING DATE: 16-JUN-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/060,031
: FILING DATE: 19-JUN-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/016,683
: FILING DATE: 19-FEB-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/896,361
: FILING DATE: 13-AUG-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: Kurt G. Briscoe
: REGISTRATION NUMBER: 33,141
: REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 332-1700
: TELEFAX: (914) 332-1844
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3461 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-468-856B-6

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Alignment Scores:
Pred. No.: 1.2e-07 Length: 3461
Score: 185.00 Matches: 130
Percent Similarity: 34.65% Conservative: 80
Best Local Similarity: 21.45% Mismatches: 200
Query Match: 6.84% Indels: 196
DB: 3 Gaps: 31

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US-09-937-636-3 (1-512) x US-08-468-856B-6 (1-3461)

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QY 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheThrPheArg 24
DB 127 CTGCTCACAGCCTCTCTCTA-----ACCTCTGGAGACCGC 162
QY 25 ValGlnGluSerValMetValProGlnGlyLeuCysIleSerValPro-----40
DB 163 CCCACACAGCCGACGCTACTGTAATGCATGCCATTCATGTTCCAGAGGGAAGAG 222
QY 41 -----CysSerPheSerTyrProArgGlnAspTyrPheGlySerThrProAlaTyr 57
DB 223 GTTCTTCTCTGCTGTCCACAACTGCCCCAGCAA-----CTTTT 261
QY 58 GlyTyr---TyrPheValAlaValThrGlnThrThyGlyAlaProValAlaThrAsn 76
DB 262 GGTCTACAGCTGGTACAAAGG-----GAAAGAGTGGATGG-----297
QY 77 HisGlnSerArgGluValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96
DB 298 -----AACCGTCAATTTAGATATGCAATAGCAATCAACAAACCAACCTACCCAGGCC 351
QY 97 AlaIysGly-----AsnCysSerLeuValIleArgAspAlaGln 109
DB 352 GCAAAACAGCGGTGAGAGACAATATACCCCAATGCATCCCTGCTGATCCAGAACTGACAC 411
QY 110 MetGlnAspGluSerGlnTyrPhePheArgValGlnArgGlySerTyrValArgTyrAsn 129
DB 412 CAGATGACACAGGATTTACACCTCTACAGTC-----ATAAGTCAAGAT 456
QY 130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149

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DB 457 CTTGTCAATGAA-----GAAGCAACTGACAGATTTCATGTATAC 495
QY 150 IleProGlnThrLeuGluProGlnProValThrValIleCysValIleAsnThrAla 169
DB 495 -----495
QY 170 PheGlnGluCysProProProSerPheSerThrThrGlyAlaAlaLeuSerSerGlnGly 189
DB 496 ---CCGGACCTGCCAAGCCCTCC-----ATCTCCAGCAACAC 531
QY 190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAsnHis 209
DB 532 TCCACCCCTGTGGAGACAAAGATGTGTG---GCTTCACTCGTGAACCTGAGACTGAG 588
QY 210 AspThrAspLeuThrCysHisValAspPheSerArgGlyValSerAlaGlnArgThr 229
DB 589 GACACAACTTACTGTGTGATAAACAATACAGACCTCCCGCTCAGTCCC-----639
QY 230 ValArgLeuArgValAlaTyrAlaProArgAspLeu---ValIleSerIleSerArgAsp 248
DB 640 ---AGGCTCAGCTGTCAATGGAACAGACCCCTACTCTACTCAGTGTCAACAGAAAT 696
QY 249 AsnThrProAspProProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThr---267
DB 697 GACACAGACCCCTATGATGTTGAATACAGAACCCAGTGAAGT---GCAAACTCCAGTAC 753
QY 268 ---ValLeuGlnAsnLeuGlnGlyThrSerLeuProValLeuGlu-----282
DB 754 CCAGTCACCTTGATGCTCATGTATGCGCGGACACCCCACTTCCCTTCAGACACC 813
QY 283 -----GlyIleSerLeuCysLeuValCysValThrHisSerSerProProAla 298
DB 814 TATTACCGTCCAGGGGCAAACTCAGCTCTCTGCTATGACACCTCTAACCCACTGCA 873
QY 299 ArgLeuSerThrThrGlnArgGlyGlnValLeuSerProSerArgProAspProGly 318
DB 874 CAGTACTCTGCTGTTTCATATGACATTCACAGCAACAGCAACAAAG-----921
QY 319 ValLeuGlnLeuProArgValGlnValGlnHisGlnGlyLeuPheThrCysHisAlaArg 338
DB 922 ---CTCTTATCTCCCTTAACATCATGTGAATATAGTGAATCCATCTCCAGCCGCAAT 978
QY 339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTyrLysGly 357
DB 979 AACTGACGTGAGCTGCAACAGACCAACAGTC-----AAGACG 1017
QY 358 LeuIleSerThrAlaPheSer-----364
DB 1018 ATCATATGTCACGTAGCTAAGTCCAGTAGAGCAAAAGCCCAATCAAAAGCAGACAGACC 1077
QY 365 -----AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAla 382
DB 1078 ACAGTCCACAGAGATAGAGCACTGTGCAACCTGACC-----TGCCTCCACA 1122
QY 383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrPro 399
DB 1123 AATGACACTGGAATTCCTCATCTCCGTGTTCTTAAAAACCAAGAGTCTCCGCTCTGGAG 1182
QY 400 ArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnValAlaPro-----417
DB 1183 AGGATGAGCTGTCCAGGCAACACACCCCTCAGC---ATAAACCTGTCAAGAGGAG 1239
QY 418 -----ThrAlaGlyPro 421
DB 1240 GATGCTGGAGCGTATTGTTGTGAGCTTTCACAAACCAATAGTAAGAACAACCAAGCCGCC 1299
QY 422 LeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuProPro 441
DB 1300 ATCATGCTGAAGCTAAACTATATATGCTTACCAAA-----GAAATAGGCTCTGACCT 1353
QY 442 GlyAla-----443

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Db	1354	GGGGCGATTGCTGGCATGTGATTGAGTACAGGCCCCGTTGGCTCTATAGCACTACC	1413
Oy	444	-----ProSerProGluSerLysLysAsn	451
Db	1414	CTGGCAGTCTTTCTGCATTTCCGGAGACCGCGGACGGGCACGACCGCTGATCTCACA	1473
Oy	452	GLuLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGln-----	469
Db	1474	GAGCAACAA-----CCCTCAGCTCTCCACACACACCTCAGGACCAC	1512
Oy	470	AlaIleProGluSerGlnGluSerGlnGluLeuHisTyrAlaThrLeuAsnPheProGly	489
Db	1513	TCCAATGACCCACCTAACACAGATGAATGAATTTACTTATTTCTACCCCTGCACTTTGAAGCC	1572
Oy	490	ValArgPro---ArgProGluAlaAlaArgMetProLys-----GlyThrGlnAlaAspTyr	506
Db	1573	CAGCAACCCACACACACCACTTCAGCGCTCCCATCTCCTAACAGCCACAGAAATATTTAT	1632
Oy	507	AlaGluValLysPheGln	512
Db	1633	TCAGAGCTAAAAAAGCAG	1650

RESULT 13
 : US-08-468-859A-6
 : Sequence 6, Application US/08468859A
 : Patent No. 6022958
 :
 : GENERAL INFORMATION:
 : APPLICANT: Barnett, Thomas; Elling, James; Kamarrck, Michael,
 : APPLICANT: Kretschmer, Axel
 : TITLE OF INVENTION: CDNA5 CODING FOR MEMBERS OF THE
 : TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
 : NUMBER OF SEQUENCES: 14
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Sprung Horn Kramer & Woods
 : STREET: 660 White Plains Road
 : City: Tarrytown
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10591-5144
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: diskette, 3.50 inch, 2.0 Mb storage
 : COMPUTER: APPLE MACINTOSH 6500
 : OPERATING SYSTEM: SYSTEM 7.5
 : SOFTWARE: Wordperfect 3.5
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/468,859A
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: 435
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/027,974
 : FILING DATE: 08-MAR-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/760,031
 : FILING DATE: 13-SEP-1991
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/274,107
 : FILING DATE: 21-NOV-1988
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/207,678
 : FILING DATE: 16-JUN-1988
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/060,031
 : FILING DATE: 19-JUN-1987
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/016,683
 : FILING DATE: 19-FEB-1987
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 06/966,361
 : FILING DATE: 13-AUG-1986
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kurt G. Briscoe
 : REGISTRATION NUMBER: 33,141
 : REFERENCE/DOCKET NUMBER: MOI 242.9-KGB

```

? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (914) 332-1700
? TELEFAX: (914) 332-1844
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3461 nucleotides
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-468-859A-6

Alignment Scores:
Pred. NO.: 1.2e-07
Score: 185.00
Percent Similarity: 34.65%
Best Local Similarity: 21.45%
Query Match: 6.84%
DB: 3

Length: 3461
Matches: 130
Conservative: 80
Mismatches: 200
Indels: 196
Gaps: 31

```

US-09-937-636-3 (1-512) x US-08-468-859A-6 (1-3461)

QY	5	LeuLeuLeuSerLeuSerLeuGlyGlySerGlnAlaMetAspGlyAlaArgPheIleArg	24
Db	127	CTGCTCAGACGCTCACTTCTA-----ACCTTCTGGACCCG	165
QY	25	ValGlnGlnSerValMetValProGlnGlyLeuCysIleSerValPro-----	40
Db	163	CCACACACTGCCCCAGCTCACTACTGATCAATGCATTCATCAATGATGGCAGAGGGAGAG	222
QY	41	-----CysSerPheSerIleYrProAlaGlnAspTrpIlnGlySerThrProAlaTyr	57
Db	223	GTTCTTCTCTCTGTCCTGTCACCAATCTGCCGCCAGCAA-----CTTTT	261
QY	58	GlyTyr-----TrpPheLeuAlaValThrGlnThrThrIleGlyAlaProValAlaThrAsn	76
Db	262	GGCTACAGCTGTGTCAAAGG-----GAAAGCTGGATGCC-----	297
QY	77	HisGlnSerArgGlnValGlnMetSerThrArgGlyAlaArgPheGlnLeuThrGlyAspPro	96
Db	298	-----AACCGTCAATTTGTAGATATGGAAATAGCAATCAACAAGCTACCCGAGGGCC	351
QY	97	AlaValGlyI-----AsnCysSerLeuValIleArgAspAlaGln	109
Db	352	GCAACACAGCGGTGAGAGACAATATACCCCAATGCATCGCTGATGATCCAGAAAGCTACCC	411
QY	110	MetGlnAspGlnSerGlnTyrPhePheArgValGlnAlaGlySerTyrValAlaGlyAsn	129
Db	412	CAGATGACACAGAGATTCTACACCTCAACAGCT-----ATAAATCGAT	456
QY	130	PheMetAsnAspGlyPhePheLeuLeuValThrAlaLeuThrGlnIleProAspValTyr	149
Db	457	CTTGTGAATGAA-----GAAGCAACTGGACAGTTCCATGTTATC	495
QY	150	IleProGlnThrLeuGlnProGlyGlnIleProValThrValIleCysValPheAsnTrpAla	169
Db	495	-----	495
QY	170	PheGlnGlnCysProProPheSerPheSerThrPheGlnAlaAlaLeuSerSerGlnGly	189
Db	496	---CCGAGACTGCCAAGCCTCC-----ATCTCCACCAACAC	531
QY	190	ThrIlePheProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAsnHis	209
Db	532	TCCACCCCGTGGAGAGACAAGAGTCTGTG---GCCTTCACTGTGAACCTGAAGTACAG	588
QY	210	AspThrAspLeuThrCysHisValAspPheSerArgIleGlyGlnValSerAlaGlnArgThr	229
Db	589	GACACAACTCACTGTGGTGATAAACATCAGAGCCTCCCGGACATCCC-----	639
QY	230	ValAlaGlyLeuArgValAlaTyrAlaArgAspLeu---ValIleSerIleSerArgAsp	248
Db	640	---AAGCTGCAAGTCTTCATATGGCAACAGGACCTCTACTACATGTCACAAAGAAAT	696

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QY 249 AenThrProAspProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr----- 267
   |||||
   :|:|:|
Db 697 GACACGAGACCTATGAGTGTGAATACAGAAACCCAGTAGT---GCGAACCGCAGATGAC 753
   |||||
QY 268 ---ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu----- 282
   |||||
   :|:|:|
Db 754 CCAGTCACCTGAAATGTACATATGACCCGAGACACCCACCATTTCCCTTCAGACACC 813
   |||||
QY 283 -----GlyGlnSerLeuGlyValGlyValThrHisSerSerProProAla 298
   |||||
   :|:|:|
Db 814 TATTACCGTCCAGGGGCAACCTCAGCCCTCTCTCTATGACGCCCTTACCCACCTGCA 873
   |||||
QY 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318
   |||||
   :|:|:|
Db 874 CAGTACTCTGGCTTATCAATGACATTCACAGAACACACACAGAG----- 921
   |||||
QY 319 ValLeuGluLeuProArgValGlnValGlnHisGlyGlyLysPheThrCysHisAlaArg 338
   |||||
   :|:|:|
Db 922 ---CTCTTATCCCTTAACATCACTGTGATTAATAGTACTCTATACCTGACGCCCAAT 978
   |||||
QY 339 HisProLeu---GlySerGlnHisValSerLeuSerLeuSerValHisTrpLysGly 357
   |||||
   :|:|:|
Db 979 AACTAGTCTACTGCTGCAACAGACACAGACATC-----AAGAGC 1017
   |||||
QY 358 LeuIleSerThrAlaPheSer----- 364
   |||||
   :|:|:|
Db 1018 ATCATAGTCTAGTACCTAGTACAGTACAGAACCCCAATCAAAACACAGACAGACC 1077
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QY 383 Leu-----IleIleMetLysIleLeuProLysArgArgThrGlnThrGlnThrPro 399
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QY 400 ArgProArgPheSerArgHisSerThrIleLeuAspTrpIleAsnValAlaPro----- 417
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QY 418 -----ThrAlaGlyPro 421
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QY 422 LeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuProPro 441
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QY 442 GlyAla----- 443
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Db 1354 GGGGCCATTGTGCGATTGTATGTAGTAGTGGCCCTGTGCTGTATAGCAGTAGGCC 1413
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RESULT 14

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US-08-408-095-30
; Sequence 30, Application US/08408095
; Patent No. 585678
; GENERAL INFORMATION:
; APPLICANT: Chinadural, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOT, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,095
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1503
; US-08-408-095-30
; US-08-408-095-30 (1-512) x US-08-408-095-30 (1-2166)
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QY 176 oSerPheSerTrp-----ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrTh 194
579 CCACTTCTCTCTGAGAAATAATGGACGCTTCTGGGAGAA----- 621
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QY 234 aLaIArgAlaProArgAspLeuValIleSerIleSerArgAspAsnThrProAspProp 254
728 TGCTGTATGCACCGAGAGCTGCGTGTCCATGACCGCGGGAGC----- 774
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QY 274 snGlyThrSerLeuProValLeuGluGlnSerLeuCysLeuValCysValThrHis 294
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QY 294 eSerProProAlaArg-----LeuSerTrpThrGlnArgGlyGlnValLeuS 310
821 CCAAGCTCCCTCCGCTCCACCTACACCTGGTTGACTGAATTAACCA----- 867
QY 310 erProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnHis 330
868 -----AGCTCCGCCACACAGCCAGAGAGTGCATGTTGAGCCGTTGAAGTCCAGCACT 922
QY 330 luGlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSer 349
923 CGGGTGGCTACTGATGCCAGGGGACCAACAGTGTGGGCAAGGCGCTTCCGCTCTCAGCA 982
QY 350 --LeuSerValHisTyrLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheL 369
983 CCTTACTGTCTACTATAGCCCGAGACCAATC-----GGCAGCGCAG 1024
QY 369 euGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIle 388
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QY 389 -----LeuProLysArg-----ArgThrGlnThrGluThr----- 398
1073 GTGGGCTCAAGCTCCACGAGCTTGGAAAGAGGACAGAGCCAGGCGCTTCAGAGAGA 1132
QY 399 -----ProArgProArgPheSerArgHisSerThrIleLeuA 411
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QY 450 -----LysAsnGlnL 453
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1411 -----GATGAGGGGATTCATCTAGACTGATCCAGTTTGGCGTCG 1453
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RESULT 15
US-09-638-649-6
Sequence 6, Application US/09638649
Patent No. 6563015
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
FILE REFERENCE: 0575/62175
CURRENT APPLICATION NUMBER: US/09/638, 649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1348
TYPE: DNA
ORGANISM: Murine
US-09-638-649-6
Alignment Scores:
Pred. No.: 4,24e-07 Length: 1348
Score: 172.50 Matches: 101
Percent Similarity: 33.95% Conservative: 46
Best Local Similarity: 23.33% Mismatches: 139
Query Match: 6.37% Indels: 147
Gaps: 21
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QY 120 Val-----GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeu 137
303 GCACCTAACAGCGGAGGAGGAGGAGGAGTCAAGTCAATACCA-----GTC 347
QY 138 LysValThrAlaLeuThrGlnLysProAspValTyrIleProGluThr-----LeuGluPro 156
348 CGAGTCTACAGATTCCTGGAGGACGAAATTTGTGATCTGCTGTAACCTGACAGCC 407
QY 157 GlyGlnProValThrVal-----IleCysValPheAsnTrpAlaPheGluGluCysProPro 175
408 AGTGTCCCTAATAGGTGGGACATGTGTCTGTAAGGAAAGCTAC-----CTGCA 458
QY 176 ProSerPheSerTrp-----ThrGlyAlaAlaLeuSerSerGlnGlyThrLys----- 191
459 GGGACCTTATGCTGCACTTAAGATGGAACTTGTATTCGCCATGGCAAAAGAAACATC 518
QY 192 -----ProThrThrSerHisPheSerValLeuSer-----Phe 202
519 GTGAGAGAGAGACAGAGACACCTGAGCGGAGCTTTTACATGCGGTGAGAGCTG 578
QY 203 ThrProArgPro--GlnAspHisAspThrAspLeuThrCysHisValAspPheSerArg 221
579 ACAGTATCCCAACCCAGAGAGAGAACCAACCATCTACTTCTCTGCAAGTTTCAAGC--- 635
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Oy	342	glyserclnhivalserleuserleuservalhistyr- - - - -	354
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Job time : 139 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 8, 2003, 20:05:43 : Search time 414 Seconds
(without alignments)
3209.042 Million cell updates/sec

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Delop 6.0, Delext 7.0

Searched: 1731049 seqs, 1297405648 residues
Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	2580.5	95.4	3024	11	US-09-910-600-27	Sequence 27, Appl
3	2576.5	95.2	2338	11	US-09-984-130-148	Sequence 148, Appl
4	2278	84.2	2265	10	US-09-910-600-1	Sequence 1, Appl
5	2265	83.7	2764	10	US-09-978-295A-258	Sequence 258, Appl
6	2265	83.7	2764	10	US-09-978-697-258	Sequence 258, Appl
7	2265	83.7	2764	10	US-09-978-192A-258	Sequence 258, Appl
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32	2265	83.7	2764	12	US-10-199-672-117	Sequence 117, Appl
33	2265	83.7	2764	12	US-10-187-749-117	Sequence 117, Appl
34	2265	83.7	2764	12	US-10-194-457-117	Sequence 117, Appl
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36	2265	83.7	2764	12	US-10-184-642-117	Sequence 117, Appl
37	2265	83.7	2764	12	US-10-196-747-117	Sequence 117, Appl
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42	2265	83.7	2764	12	US-10-173-694-117	Sequence 117, Appl
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ALIGNMENTS

RESULT 1
US-09-910-600-15
Sequence 15, Application US/09910600
Publication No. US2003003631A1
GENERAL INFORMATION:
APPLICANT: Longphre, Malinda
APPLICANT: Chang, Han
TITLE OF INVENTION: NOVEL SINGLETS AND USES THEREOF
FILE REFERENCE: D0003NP
CURRENT APPLICATION NUMBER: US/09/910,600
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 15
LENGTH: 2208
TYPE: DNA
ORGANISM: Homo sapiens
US-09-910-600-15

Alignment Scores: 5.01e-253 Length: 2208
Pred. No.: 2580.50 Matches: 510
Score:

Not Recd At

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QY 396 ThrGluThrProArgProArgPheSerArgHisSerThrIleuAspTyrIleAsnVal 415
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Db 1929 GTCCCGAGCGCTGGCCCCCTGCTCAGAGCGAATGAGAAAGCCACACCAACAGCTCT 1968
QY 436 ArgThrProLeuProProGlyAlaProSerProGluSerLysAsnGlnLysGln 455
Db 1989 CGGACCCCTCTTCCACACAGGTGCTCCCTCCCGCAGATCAAGAAAGAAACCAAAAAAGAG 2048
QY 456 TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGln 475
Db 2049 TATGAGTGGCCAGATTCTCCAGAACCCAAATCATCTCAAGCCCAAGATCCAGAGAG 2108
QY 476 SerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgProGlu 495
Db 2109 AGCCAAAGAGAGCTCTCATATGACACGCTCACTTCCAGGCGTCAGACCCAGGCGTAG 2168
QY 496 AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512
Db 2169 GCCCGAGTGGCCAGAGGCGACCCAGCGGATTATGCAGAGCAGATTCCTCA 2219

RESULT 3

US-09-984-130-148

Sequence 148, Application US/09984130

Publication No. US20030055231A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OR INVENTION: 12 Human Secreted Proteins

FILE REFERENCE: PF489P2

CURRENT APPLICATION NUMBER: US/09/984,130

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 60/243,792

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: 09/836,353

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/198,407

PRIOR FILING DATE: 2000-04-19

PRIOR APPLICATION NUMBER: PCT/US99/25031

PRIOR FILING DATE: 1999-10-27

PRIOR APPLICATION NUMBER: 60/105,971

PRIOR FILING DATE: 1998-10-28

NUMBER OF SEQ ID NOS: 149

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 148

LENGTH: 2338

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (3)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (6)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (9)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (11)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (12)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE

LOCATION: (17)

1024e)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (18)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (21)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (33)
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LOCATION: (34)
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NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (38)
OTHER INFORMATION: n equals a,t,g, or c
US-09-984-130-148

Alignment Scores:
Pred. No.: 1.39e-252 Length: 2338
Score: 2576.50 Matches: 509
Percent Similarity: 73.17% Conservative: 1
Best Local Similarity: 73.03% Mismatches: 2
Query Match: 95.21% Indels: 185
Gaps: 2

US-09-937-636-3 (1-512) x US-09-984-130-148 (1-2338)

QY 1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20
Db 201 ATGCTACTGTCACACTGCTGCTGCTCTCTGCGGGGCTCCAGGCTATGATGGAGGA 260

QY 21 PheTrpIleArgValGlnGlnSerValMetValProGluLysLeuCysIleSerValPro 40
Db 261 TTCTGATACGATGCAAGAGATGATGATGTCCTCCGAGGCGCTGTGCTCTGTGCCC 320

QY 41 CysSerPheSerTyrProArgGlnAspTyrThrGlySerThrProAlaTyrGlyTyrTrp 60
Db 321 TGCTCTTTCTCCACCCCGCAAGACTGACAGAGGCTACCCAGCTTATGCTACTG 380

QY 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
Db 381 TTCAAGACAGTACTGAGACCAACCAAGGGGTCTGTGTGCCCAACCAACCAAGAGTGA 440

QY 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
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 Db 441 GAGGTGGAAATAGACCCGGGGCCATTCCAGCTACTGGGATCCCGCAAGGGGAAC 500
 QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnIlePhePheArgVal 120
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 Db 501 TCCTCTTGTTGGTATGACAGACGGCAGATGACAGAGTCAACAGTCTCTTTCGGGGT 560
 QY 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
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 Db 561 GAGAGGGAGAGCTATGTGAGATATATTTCATGACAGATGGGTCTTCTTAAAGTAACA 620
 QY 141 AlaLeuThrGlnLysProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal 160
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 Db 621 GCCCTACTCAGAACCTTATGTCTTCACTCCCGAGACCTGGAGCCCGGGAGCCGGT 680
 QY 161 ThrValIleCysValPheAsnTrpAlaPheGlnGluCysProProSerPheSerTrp 180
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 Db 681 ACGGTACTGTGTGTAACTGGGCTTGAAGAAATGTCCACCCCTTCTTCTCTGG 740
 QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
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 Db 741 ACGGGGGTGGCCCTCTCTCCCAAGAACCAACCAACCACTCCCACTCTCAGTGC 800
 QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
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 Db 801 ACCTTCAGGCCCAAGACCCAGGACCCACAAACAGACCTCCATGCTGAGCTTCTCC 860
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 Db 861 ACAAAGGGGTGTAGGCTACAGAGACCGTCCGACTCCGTGGCTATGCCCCAGAGAC 920
 QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
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 Db 921 CTGTGTATCAGATTTCACGTGACACACAGCCAGCCCTGGAGCCCAAGCCCAAGGAAAT 980
 QY 252 ----- 252
 Db 981 GTCCCATACCTGGAAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTCTGTGACAGC 1040
 QY 252 ----- 252
 Db 1041 CAGCCCTCTGCACACTGAGCTGGGTCTGACAGAACAGATCTCTCTGTCCATCCC 1100
 QY 252 ----- 252
 Db 1101 TGGGGCCCTAGACCCCTGGGCTGAGACTGCCCGGGGTGAAGGCTGGGATTCAGGGCCG 1160
 QY 252 ----- 252
 Db 1161 TACACCTGCGAGCGGAGAACAGGCTTGGCTCCACAGCAGGAGCCCTGGACCTCTCTGTG 1220
 QY 253 -----PROProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
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 Db 1221 CAGTATCTCTCCAGAGAACTGAGAGTGTTCCTCCAGCAAAACAGCAGCTCGGAA 1280
 QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlnSerLeuLysValCys 290
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 Db 1281 AACCTTGGAGACGGCAGTCTCTCCAGTACTGGAGGGCAAAAGCCCTGTGCTGTCTGT 1340
 QY 291 ValThrHisSerSerProProAlaArgLeuSerTyrThrGlnArgGlyGlnValLeuSer 310
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 Db 1341 GTCACACACAGCAGACCCCGCAGCAGCTGAGCTGACCCAGAGGGGACAGTTCGAGAC 1400
 QY 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330
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 Db 1401 CCCTCCACAGCTCAAGACCCCGGGGTCTGAGACTCCCTCGGGTTCAATGAGACGAA 1460
 QY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
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 Db 1461 GAGAGATTCACTGACAGCTGGCAGCCACCTGGGCTCCACACAGCTCTCTCTCAGACCTTC 1520

QY 351 SerValHisTyr----- 354
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 Db 1521 TCCGTCACTACTCCCCGAAAGCTGTGGGCCCTCTCTGCTCTGGAGGCTCAGGCTCTG 1580
 QY 354 ----- 354
 Db 1581 CACTGACGTCCTCCAGAGCCAGCCGCCCTCTCTGTGGCTGTGGGGAG 1640
 QY 354 ----- 354
 Db 1641 GAGCTGTGAGGGGGAACAGACAGACTCTCTGAGGTACACCCCACTCAGCCGG 1700
 QY 354 ----- 354
 Db 1701 CCCTGGGCAACAGCTCCCTGAGCTTCATGAGGGCTAGCTTGCTGAGCTCCGC 1760
 QY 355 -----Lys 355
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 Db 1761 TGTGAGGCTGGAACTCCATGGGGCCAGAGTGGATCCATCTGCACTGCGCAGATTAAG 1820
 QY 356 LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla 375
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 Db 1821 AAGGACTATCTCAACGGCATTTCTCAACGGAGCGTTCTGGGAATCGGCATCAGCGCT 1880
 QY 376 LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuProLysArgArgThrGln 395
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 Db 1881 CTTCCTTCTCTGCTGCTGGCCCTGATCATCATGAAATTTCTACCGAAGAGAGACTCAG 1940
 QY 396 ThrGluThrProArgProArgPheSerArgHisSerThrIleLeuAspTyrIleAsnVal 415
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 Db 1941 ACAGAAACCCCGAGGCCAGGTTCTCCGGCAGACAGCATCTCGATTATCATCATGTG 2000
 QY 416 ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro 435
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 Db 2001 GTCCGACGGCTGGCCCTCTGCTCAGAAAGGGAATCAAAAGCCACACCAACACTCTCT 2060
 QY 436 ArgThrProLeuProGlnLysAlaProSerProGlnSerLysLysAsnGlnLysGln 455
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 Db 2061 CGGACCCCTTCCACACAGGTGCTCTCCCGCATCAAAAGAACCAAGAAAGGCGAG 2120
 QY 456 TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGlnGlu 475
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 Db 2121 TATCAGTTCGCCAGTTTCCAGAACCAATCATCTCACTCAAGCCCAAAATCCAGAG 2180
 QY 476 SerGlnGluGlnLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgProGlu 495
 |||||
 Db 2181 AGCCAAAGAGAGCTCCATTATGCGACGCTCACTCACTCCAGGGCTCAGACCGGCTGAG 2240
 QY 496 AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512
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 Db 2241 GCCCGGATGCCCAAGGGCAACCCAGCGGATTTATGCAAGTCAAGTTCCA 2291
 RESULT 4
 US-09-910-600-1
 ; Sequence 1, Application US/09910600
 ; Publication No. US20030036631A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Longphre, Malinda
 ; APPLICANT: Chang, Han
 ; APPLICANT: Whitney, Gene
 ; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
 ; FILE REFERENCE: D0003NP
 ; CURRENT APPLICATION NUMBER: US/09/910,600
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 60/220,139
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2565
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-910-600-1

Alignment Scores:

Prod. No.:	4.24e-222	Length:	2565
Score:	2278.00	Matches:	452
Percent Similarity:	75.25%	Conservative:	1
Best Local Similarity:	75.08%	Mismatches:	1
Query Match:	84.18%	Indels:	148
DB:	11	Gaps:	2

US-09-937-636-3 (1-512) x US-09-910-600-1 (1-2565)

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QY 1 MetleuLeuProleuLeuLeuSerSerleuLeuGlyGlySerGlnAlaMetAspGlyArg 20
Db ATGCTACTGCGCAGCTGCTGCTCTGCTGCTGCGGCGGTCCAGGCTATGATGGAGGA 188
QY 21 PheTrpIleArgValGlnGlnSerValMetValProGlnGlyLeuGlyIleSerValPro 40
Db TTTCTGGATACGAGTGGAGGAGTCAGTGTGGTGGGCGCTGTGCATCTCTGTGCC 248
QY 41 CysSerPheSerTyProArgGlnAspTrpThrGlySerThrProAlaTyArgTyrTrp 60
Db TGCCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 308
QY 61 PheLysAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
Db TTCAAGCAGTCACTGAGACACCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 368
QY 81 GlnValGlnMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
Db GAGGTGGAATGAGACCCCGGGGCGGATCCAGCTCTGCGGATCCCGCCAGGGGAGAC 428
QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal 120
Db TGCCTCTGTTGGATCAGAGACGGCAGATGCAAGATAGTCACTACTTCTTCGGGTG 488
QY 121 GlnArgGlySerTyValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
Db GAGGAGGAGAACTGTGAGATATATATTCATGACAGATGGTCTTCTTAAAGTAAACA 548
QY 141 AlaLeuThrGlnLysProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal 160
Db 548 ----- 548
QY 161 ThrValIleCysValPheAsnTrpAlaPheGlnGlnCysProProPheSerPheSerTrp 180
Db 548 ----- 548
QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
Db 549 -----GTGCTC 554
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
Db AGCTTACGCCCAACCCAGACGACACACACACACACCTCACTCATGTGATGCTTCTCC 614
QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
Db AGAAAGGGGTGAGCGCAGACAGAGACCGCTCGACTCCGTGTGGCTATGCCCCCAGAGAC 674
QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
Db 675 CTTGTATACAGCATTTTCACTGACACACGCCAGCCCTGAGCCCCAGCCCGAGGAAT 734
QY 252 ----- 252
Db 735 GTCCCATACTGGAAGCCCAAAAGCCAGTCTCTGCGGCTCTCTGTGCTGACAGC 794
QY 252 ----- 252
Db 795 CAGCCCGCTGCACACTGAGCTGGGTCTCTGCAAGAACAGAGTCTCTCTGCTGCCATCCC 854
QY 252 ----- 252
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Db 855 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGCTGGGGATTCAGGGCCG 914
QY 252 ----- 252
Db 915 TACACCTCCGAGGGAGAACAGGCTTGGCTTCCACGACGAGCCCTGGAGCTCTGTGTG 974
QY 253 -----ProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGln 270
Db CAGTATCTCCAGAGAACCTGAGAGTGTGTTTCCAGAGAACAGAGAGCTCTGGAA 1034
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyGlnSerLeuCysLeuValCys 290
Db AACCTGGGAGCGCAGCTCTCTCCAGTACTGAGGCGCAAACTCTGCTGTCTGT 1094
QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
Db GTCAACACACAGACCCCGCCAGAGCTGAGCTGAGACCCAGAGGGGACAGTTCTGAGC 1154
QY 311 ProSerGlnProSerAspProGlyValLeuGlnLeuProArgValGlnValGlnGln 330
Db CCTTCCAGCCCTCAGACCCCGGGGCTCTGAGAGCTCTCGGTTCAAGTGGACACGAA 1214
QY 331 GlyLupPheThrCysHisAlaArgHisProLeuGlnSerGlnHisValSerLeuSer 350
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QY 351 SerValHisTyrlsLysGlyLeuIleSerThrIlePheSerAsnGlyAlaPheLeuGly 370
Db TCGGTGCACTTAAAGAGGAGCTCAATCAAGGATTTCTCAACGGAGGCTTTCTGGGA 1334
QY 371 IleGlyIleThrAlaLeuLeuPheLeuGlnLeuAlaLeuIleIleMetLysIleLeuPro 390
Db ATCGGACATCAGGCTCTTCTTCTCTCTGCTGCTGCGCCGTGATCATCATGAATCTACG 1394
QY 391 LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu 410
Db AAGAGAGGAGCTCAGACAGAAACCCAGAGGCTTCTCCGCGACAGCAGATCTG 1454
QY 411 AspTyrlIleAsnValAlaProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
Db GATTACATCAATGTGTGTCGACGCGCTGGCCCTGGCTCGAAGCGGAATCACAAGCC 1514
QY 431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlnSerLysLys 450
Db AACCAAAACAGTCTCGAGACCCCTCTCCACACAGAGTGTCTCCCTCCCAAGTCAAGAG 1574
QY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGlnLupProLysSerSerThrGlnAla 470
Db AACCAGAAAAGCAGTATCACTTGCACAGTTTCCAGAACCCCAATCATCCACTCAAGCC 1634
QY 471 ProGlnSerGlnGlnSerGlnGlnGlnIleuHisTyrlAlaThrLeuAsnPheProGlyVal 490
Db CCAGATTCACGAGAGAGCAAGAGAGGTCCATTATGCGACAGCTCACTTCCAGGGCTC 1694
QY 491 ArgProArgProGlnAlaArgMetProLysGlyThrGlnAlaAspTyrlAlaGlnValLys 510
Db AGACCCAGGCTGTAGGCGCGGATGCCCAAGGCGACCCAGGGGAGTATATGCAAGTCAAG 1754
QY 511 PheGln 512
Db 1755 TTCCAA 1760
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RESULT 5
US-09-978-295A-258
Sequence 258, Application us/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Mel-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-03-10
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PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-13
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29


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Db      1252 ATGGCATTCACGGCTCTTTCTTCTGCTGCGCTGATATCATGAGATTCACGC 1311
QY      391 LysArGArGThGlnThGlnThrProArGProArGPhSeArGHisSerThrlleu 410
Db      1312 AAGAGACGAGCTCAGACAGAAACCCGAGCGCCAGGTTCTCCGGACAGCAGATCCG 1371
QY      411 AsPTyrlleAsnValAlProThralAgIlyProleuAlaGlnLysArGsnGlnLysAla 430
Db      1372 GATTACATCAATGTGTTCCCGAGCGCTGCGCCCTGCGCTCAGAAAGCGAATCAGAAAGCC 1431
QY      431 ThrProAsnSerProArGhrProleuProProGlyAlaProSerProLuserlyslys 450
Db      1432 ACACCAACAGTCCTCGAGCCCTCTCCACCAAGGCGCTCCCTCCCAAAATCAAGAAAG 1491
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Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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APPLICANT: Pan, James;
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APPLICANT: ROY, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9,936-221	Length:	2764
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Best Local Similarity:	74.75%	Mismatches:	3
Query Match:	83.70%	Indels:	148
DB:	10	Gaps:	2

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Db 106 TTTCGGATACGACGCGCGAGATCGATGTCGCCAGGCCCTGTCATCTGTCGCC 165
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QY 61 PheIysAlaValThrGlnTrpThrGlyValAlaProValAlaTrpAsnHISGlnSerArg 80
Db 226 TTCAACGACGATGACGACACCAAGGCTCTGCGCACAAACACAGATCGA 285
QY 81 GluValGlnMetSerTrpArgGlyArgPheGlnLeuThrGlyAspProAlaTrpGlyAsn 100
Db 286 GAGGTGAATGACACCGCGCGCATTCAGCTCAGTGGATCCCGCAAGGAGAC 345
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Db 346 TGCTCTTGGTATCAGACAGCGCGCATGATGATGATGATGATGATGATGATGATG 405
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Db 406 GAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 465
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; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1997-10-17
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Query Match: 83.70% Indels: 148
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 Db 166 TCTCTTTCTCTTACCCCGACAAAGCTGGACAGGGTTCACCCAGCTTATGGCTACTGG 225
 0Y 61 PheValAlaValThrGlnThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
 Db 226 TTCAAGACAGTACTGAGACCAACCAAGGCTGCTCTGTGGCCCAACCAACAGAGTCA 285
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 Db 286 GAGGTGGAATGAGACCCGGGGCCGATTCACGTCACCTGGGGATCCCGCAAGGGAGAC 345
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 0Y 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
 Db 466 -----GTCGTC 471
 0Y 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
 Db 472 AGCTTCAGGCCAGCCAGGACCAACACACGACCTCAGCTGACATGTGACTCTCC 531
 0Y 221 ArgGlyGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
 Db 532 AGAAAGGCTGTAGCGCACAGAGACGCTCCGACTCGTGGCTATGCCGCCAGAGAC 591
 0Y 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
 Db 592 CTGTATTATCAGCATTTACAGTGCACAACAGCGCAGCCCTGAGACCCAGCCAGGGAAT 651
 0Y 252 ----- 252
 Db 652 GTCCCATACCTGGAAGCCCAAAAGGCGAGTTCTGCGGCTCTGTGCTGTGACAGC 711
 0Y 252 ----- 252
 Db 712 CAGCCCCCTGCCACACTGAGTGGGTCTGTGAGAAACAGAGTCTCTCTGTCCTATCCC 771
 0Y 252 ----- 252
 Db 772 TGGGGCCCTAGACCCCTGGGCTGAGAGTGGCCGGGGTGAAGGCTGGGGAATTCAGGGCCG 831
 0Y 252 ----- 252
 Db 832 TACACCTGCGAGCGAGAACAGGCTTGCTCCAGCAGCGAGCCCTGGACCTCTCTGTG 891
 0Y 253 -----ProGlnAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
 Db 892 CAGTATCTCTCCAGAGAACTGAGAGTGTGTTTCCCAAGCAACAGGAGCACTGCGGAA 951
 0Y 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGlnGlyGlnSerLeuCysLeuValCys 290

Db 952 AACCTTGGAGAGCGACGCTCTCCAGTACTGGAGGGCAAAAGCTGTGCTGCTCT 1011
 0Y 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310
 Db 1012 GTCACACAGACAGCCCCCAGCAGAGGCTGAGCTGAGCCAGAGAGGGAGCAGGTTCTGAGC 1071
 0Y 311 ProSerGlnProSerAspProGlyValIleuGlnLeuProArgValGlnAlaGlnHisGlu 330
 Db 1072 CCTCCAGCCCTCAGAACCCCGGGGTCTGGAGTCTGCTGGGGTTCMACTGAGCAGCA 1131
 0Y 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSer 350
 Db 1132 GGAGAGTTCACCTGCCACGCTGGCAGCCACCTAGGCTCCACAGAGCTCTCTCAGCCTC 1191
 0Y 351 SerValHisTrpLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
 Db 1192 TCCGTGCACTATAGAAAGGAGCTCATCTCAAGGCACTTCTCCAAAGCAGAGCTTCTGGA 1251
 0Y 371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleMetLysIleLeuPro 390
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 Db 1312 AAGAGCGGAGCTCAGACAGAAACCCGAGGCCAGGTTCTCCGGCAGACAGCATCTCG 1371
 0Y 411 AspTyrIleAsnValAlaProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
 Db 1372 GATTACATCAATGTGTCTCCGAGCGCTGCGCCCTGGCTCAGAGGGGAAATCAGAAAGCC 1431
 0Y 431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlnSerLys 450
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RESULT 8
 US-09-999-832A-258
 ; Sequence 258, Application US/0999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Flvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC3
CURRENT APPLICATION NUMBER: US/09/999, 832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-03-10
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2 PRIOR APPLICATION NUMBER: 60/084639
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4 PRIOR APPLICATION NUMBER: 60/084640
5 PRIOR FILING DATE: 1998-05-07
6 PRIOR APPLICATION NUMBER: 60/084598
7 PRIOR FILING DATE: 1998-05-07
8 PRIOR APPLICATION NUMBER: 60/084600
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10 PRIOR APPLICATION NUMBER: 60/084627
11 PRIOR FILING DATE: 1998-05-07
12 PRIOR APPLICATION NUMBER: 60/084643
13 PRIOR FILING DATE: 1998-05-07
14 PRIOR APPLICATION NUMBER: 60/085339
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17 PRIOR FILING DATE: 1998-05-13
18 PRIOR APPLICATION NUMBER: 60/085323
19 PRIOR FILING DATE: 1998-05-13
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21 PRIOR FILING DATE: 1998-05-15
22 PRIOR APPLICATION NUMBER: 60/085700
23 PRIOR FILING DATE: 1998-05-15
24 PRIOR APPLICATION NUMBER: 60/085689
25 PRIOR FILING DATE: 1998-05-15
26 PRIOR APPLICATION NUMBER: 60/085719
27 PRIOR FILING DATE: 1998-05-15
28 PRIOR APPLICATION NUMBER: 60/085580
29 PRIOR FILING DATE: 1998-05-15
30 PRIOR APPLICATION NUMBER: 60/085573
31 PRIOR FILING DATE: 1998-05-15
32 PRIOR APPLICATION NUMBER: 60/085704
33 PRIOR FILING DATE: 1998-05-15
34 PRIOR APPLICATION NUMBER: 60/085697

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Alignment Scores:

Pred. No.:	9, 93e-221	Length:	276e-450
Score:	265.00	Matches:	450
Percent Similarity:	74.93%	Conservative:	1
Best Local Similarity:	74.75%	Mismatches:	3
Query Match:	83.70%	Gaps:	148
DB:	10		2

US-09-937-636-3 (1-512) x US-09-999-832A-258 (1-2764)

QY	1	MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg	20
Db	46	ATCTACTCCCACTGCTGCTCTCCCTGGCTGGGGGGGGTCCACAGGCTATGATGGAGGA	105
QY	21	PheTrpIleArgValGlnGlnSerValMetValProGluGlyLeuCysIleSerValPro	40
Db	106	TTCTGGATACGAGTCCAGAGTCAATGATGGTGGCGAGGGCTGTGCATTTCTGTCCC	165
QY	41	CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTCTCCACCCCCGACACAGATCGACAGGGGTCTACCCAGCTTATGGCTACTGG	225
QY	61	PheIysAlaValThrGluThrThrItySglYalProValAlaAlaThrAsnHisGlnSerArg	80
Db	226	TTTCAAAAGCAGTGCATCGACCAACCAAGGGTGTCTCTGGCCACAAACACACAAAGTCGA	285
QY	81	GluValGlnMetSerThrArgIleArgIleArgPheGlnLeuThrGlyAspProAlaIysGlyAsn	100
Db	286	GAGGTGGAATGAGCCACCCGGGGCGGATTCACGCTCACTGGGGATCCCGCCAAAGGGAAAC	345
QY	101	CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal	120
Db	346	TGCTCTTGGTGATCGACAGCCGACAGATGCAGGATGATGCTACAGTACTTCTTCCGGTG	405
QY	121	GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuIysValThr	140
Db	406	GAGAGAGGAGAGCATATGATATATATTTCAATGAACGATGGCTTCTTTCAAAAGTACA	465

OY	141	AlaLeuThrGlnLysProAspValIrryIleProGluThrLeuGluProGlyGlnProVal	160
Db	465	-----	465
OY	161	ThrValIleCysValAlpheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp	180
Db	465	-----	465
OY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu	200
Db	466	----- -GNGCTC	471
OY	201	SerPheThrProArgProGlnAspHisAspTrpAspLeuThrCysHisValAspPheSer	220
Db	472	AGCTTACAGCCCGACAGCCCGACAGACACACACCGACTCCACTGCCATGTGAGACTTCTCC	531
OY	221	ArgLysGlyValSerAlaGlnArgThrValAArgLeuArgValAlaArgValaProArgAsp	240
Db	532	AGAAAGGGTGTGAGGGCACAGAGAGACCGTCCGACTCCGTGTGGCTATATCCCCACAGAC	591
OY	241	LeuValIleSerIleSerArgAspAsnThrProAsp	252
Db	592	CTGTGTATCAGCATTTACAGTGACAACAGCCAGCCCTGTGAGCCCCAGCCCGAGGGAAT	651
OY	252	-----	252
Db	652	GTCCCATACCTGGAAAGCCAAAAGGCGAGTTCCTGCGGGCTCTGTGCTGCTGACAGC	711
OY	252	-----	252
Db	712	CAGCCCCCTGCCACACTGAGCTGGGTCTCTGCAGAACAGAGTCTCTCTCTGCCATGCC	771
OY	252	-----	252
Db	772	TGGGGCCCTAGACCCCTGGGGCTGGAGCGCCCGGGGTGAAGGCTGGGGATTCCAGGGGCG	831
OY	252	-----	252
Db	832	TACACCTGCGCGAGAGACAGGCTGTGCTCCACAGACGAGCCCTGACCTCTCTGTG	891
OY	253	----- PropGluLAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	270
Db	892	CAGTATCTCCAGAAACCTGAGAGTGAATGTTTCCCAAGACAAACAGGACAGCTCGGAA	951
OY	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGluGlnSerLeuCysLeuValCys	290
Db	952	AACCTGGGAAGCGGACGCTCTCCAGACTGAGGAGGCGCAAGGCTGTGCTGGTCTGT	1011
OY	291	ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	310
Db	1012	GTCACACACAGACGCCCGCCAGCGCTGACTGGACCCCAAGGAGGAGAGGTTCTGAGAC	1072
OY	311	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnHisGlu	330
Db	1072	CCCTCCCGACCCCTGAGACCCCGGGGTCTCGAGCGTCCCGGGTTCCACTGGAGCGAA	1132
OY	331	GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1132	GGAGAGTTCACCTGCCACGCTGGGACCCACACTGGGGCTCCACAGACGTCTCTCAGCTTC	1192
OY	351	SerValHisTryLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly	370
Db	1192	TCCGTGCACTATTAAGAAGGACTCATCTCAAGGGCATTTCTCAAGGAGCGATTCTGGGA	1252
OY	371	IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro	390
Db	1252	ATCGGCATCAGCGGCTCTTCTTCTCTGCTGCGCCCTGATCATCATGAAGATTCTACCG	1312
OY	391	LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu	410
Db	1312	AAGAGACGGACTCACACAGAAACCCCGAGGCCAGGTTTCTCCGGACAGCGAGTCTCG	1372
OY	411	AspTryIleAsnValValProThrIaGlyProLeuAlaGlnLysArgAsnGlnLysAla	430

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Db 1372 GATTACATCATGTGTCGCCAGCGCTGGCCCCCTGGGCTCGAAGCGGAATCAGAAAGCC 1431
QY 431 ThrProInsSerProArgThyProLeuProProGlyAlaProSerProGlySerLysLys 450
Db 1432 ACACCAACAGCTCTCGAGCCCTCTCCACACAGAGTCTCTCCAGAAATCAAGAG 1491
QY 451 AsnGlnLysLysGlnTyrglnLeuProSerPheProGlyProLysSerSerThyGlnAla 470
Db 1492 AACCAAGAAAAGAGCTATCATGTTGCCAGATCCCAATCATCTCAAGCC 1551
QY 471 ProGlnSerGlnLysGlnGlnLeuHisTyraAlaThrLeuAsnPheProGlyVal 490
Db 1552 CCAGAAATCCAGAGAGACCAAGAGAGACTCCATATGCGACGCTCAACTCCAGCGCTC 1611
QY 491 ArgProArgProGlnAlaArgMetProLysGlyThyThrGlnAlaAspTyraAlaGluValLys 510
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QY 511 PheGln 512
Db 1672 TTCCAA 1677
RESULT 9
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; Sequence 258, Application US/09978189
; Publication No. US2003004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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OY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
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DB 532 AGAAAGGGTGTGAGCGCACAGAGACCGCTCCGACTCCGTGCGCTATGCCCCAGAGAC 591
OY 241 LeuValIleSerIleSerArgAspAsnTrpProAsp ----- 252
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DB 592 CTGTGTATCAGCATTTTCAGTGTACACACGCCAGCCCTGAGCCCGCCAGCCAGGGAAT 651
OY 252 ----- 252
DB 652 GTCACATACGTGGAGCCCAAAAGGCCAGTTCCTGCGGCTCTCTGTCCTGCTACAGAC 711
OY 252 ----- 252
DB 712 CAGCCCTGCGCACACTGAGTGGGTCTCTGACAAACAGATCCTCTGCTGCCATCCC 771
OY 252 ----- 252
DB 772 TGGGGCCCTAGACCCCTGGGCTGAGCTGCCCGGGGTGAAGCTGGGATTCAGGGCCG 831
OY 252 ----- 252
DB 832 TACACCTGGCGGAGGAGAACAGGCTTGGCTCCACAGACGACCCCTGAGACTCTCTGTC 891
OY 253 -----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
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DB 892 CAGTATCCTCCAGAGAACCTGAGATGATGTTTCCCAAGCAAAACAGACAGTCTGGAA 951
OY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlnGlnSerLeuGlyValCys 290
    |||||
DB 952 AACCTTGGGAAAGGAGCTCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTCTGT 1011
OY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyValInValLeuSer 310
    |||||
DB 1012 GTCAACACACAGAGCCCGCCAGCCAGGCTGAGCTGAGCCACAGAGGAGAGTTCTGAGC 1071
OY 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnHisGlu 330
    |||||
DB 1072 CCGTCCAGCCCTCAGACCCCGGGGCTCTGAGCTGCGCGGGTCAAGTGAAGACAGCA 1131
OY 331 GylGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
    |||||
DB 1132 GGAGAGTTACCTGCGACGCTGGGACCCACACTGGGCTCCACACAGCTCTCTCAGCCTC 1191
OY 351 SerValHisTyrLysGlyLeuLeuSerThrAlaPheSerAspGlyValAlaPheLeuGly 370
    |||||
DB 1192 TCCGTCGACATATAAAGGAGACTCATCTCAACGGCATTTCTCAAGGAGAGCTTTCTGGGA 1251
OY 371 IleGlyIleThrAlaLeuLeuPheLeuGlyLeuAlaLeuIleIleMetLysIleLeuPro 390
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DB 1252 ATCGGCATCAGCGGCTCTCTCTTCTCTGCTGCGCGCTGATCATCATGAAGATTCACCG 1311

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OY 391 LysArgArgThrGlnThrGlnThrProArgProArgPheSerArgHisSerThrIleLeu 410
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DB 1312 AAGAGCGGAGCTAGACACAAACCCCGAGGCCCCAGGTTCTCCCGGACAGCAGATCTCG 1371
OY 411 AspTyrIleAsnValAlaProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
    |||||
DB 1372 GATTACATCATATGTGTTCCCGAGCGGTGGCCCTCTGCTGCTCAGAGGGAATCGAAAGCC 1431
OY 431 ThrProAsnSerProArgTrpThrProLeuProProGlyAlaProSerProGluSerLys 450
    |||||
DB 1432 ACACCAAAAGTCTCGAGACCCCTCCTCCACAGGTCGTCCCTCCAGAAATCAAGAGG 1491
OY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
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DB 1492 AACCAAGAAACAGATATCAGTTGCCAGTTTCCAGAAACCCAAATCATCTCACTCAAGCC 1551
OY 471 ProGluSerGlnGluSerGlnGluLeuLeuHisTyrAlaThrLeuAsnPheProGlyVal 490
    |||||
DB 1552 CCAGAAATCCAGAGAGAGCCCAAGAGAGCTCATTTATGCCAGCTCAACTTCCAGGCTC 1611
OY 491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510
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DB 1612 AGACCCAGGCTGAGGCGCGGATGCCCAAGGAGGACCCAGGAGATTATGCAAGATCAAG 1671
OY 511 PheGln 512
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RESULT 11
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; Sequence 258, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 258
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US-09-978-585A-258

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APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Goddard, Audrey
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APPLICANT: Kijavini, Ivar J.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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40 PRIOR APPLICATION NUMBER: 60/085573
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42 PRIOR APPLICATION NUMBER: 60/085704
43 PRIOR FILING DATE: 1998-05-15
44 PRIOR APPLICATION NUMBER: 60/085697

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Alignment Scores:	
Pred. No.:	9,936-221
Score:	2285.00
Percent Similarity:	74.928
Best Local Similarity:	74.758
Query Match:	83.708
DB:	11
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	Length: 2764
	Matches: 450
	Conservative: 1
	Mismatches: 3
	Indels: 148
	Gaps: 2

QY	1	MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg	20
Db	46	ATGCACTACCCACTGCTGCTGCTCCCGGCGGGGGGCTCCAGCGCTATGATGGAGGA	1050
QY	21	PhetPrIAlaValAlGlnGlnSerValMetValProGlnGlyLeuCysIleSerValPro	40
Db	106	TTCGTGATTCAGAGTCGACGAGTCATGTATGGCGCGGAGCGCTGTGATCTGTGCCCC	1650
QY	41	CysSerPheSerTyrProArgGlnAspPrpPheGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTTCTCTACCCCGGACAAACCTCGACAGGGGTCTACCCAGCTTAGGGCTACTGG	2253
QY	61	PheIysAlaValThrGluThrThrIysGlyAlaProValAlaThrAsnHisGlnSerArg	80
Db	226	TTCAAAAGCATGACTGAGCAACAACAAAGGTGCTCTGTGGCCACAACACACAAAGTCGA	2853
QY	81	GluValGluMetSerThrArgGlyIyrpPheGlnLeuThrGlyAspProAlaIysGlyAsn	100

Db	286	GAGGTGGAATGAGCACCCGGGGCCATTCCAGCTACTGCTGGGATCCCGCAAGGGAAAC	345
OY	101	CysSerLeuValILleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal	120
Db	346	TGCTCTTGGGATCAGACAGCGCGAGATCAGAGATGAGCACAGTACTCTTCGGGATG	405
OY	121	GluArgGlySerTyrValArgTyrAspPheMetAspAspGlyPhePheLeuValThr	140
Db	406	GAGGAGGAAGACTGATGTGACATTAATTTATATAGACAGTGGGTTCTTTATAAAGTAAACA	465
OY	141	AlaLeuThrGlnIysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal	160
Db	465	-----	465
OY	161	ThrValIleCysValPheAsnTTPAlaPheGluGluCysProProSerPheSerTTP	180
Db	465	-----	465
OY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValIleu	200
Db	466	-----GTGCTC	471
OY	201	SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	220
Db	472	AGCTTCACGGCCGACAGCCCCAGAGCCAAACACCGACCTCAGCTGCATGTGGACTTCGC	531
OY	221	ArgGlySerGlyValSerAlaGlnArgTThrValArgLeuArgValAlaLeuThrLaaProArgAsp	240
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OY	241	LeuValIleSerIleSerArgAspAsnThrProAsp-----	252
Db	592	CTTGTTATCAGCATTTTCAGCTGACAAACAGCCAGCCCTGGAGCCCAAGCCCAAGGAAAT	651
OY	252	-----	252
Db	652	GTCCCATACCTGGAGAGCCCAAAAGGCCAGTTCCTGGGCTCCTGTGCTGTGACAGC	711
OY	252	-----	252
Db	712	CAGGCCCTGCCACACTGAGCTGGGTCCTGACAGAACAGAGTCTCTCCGTCCCATCCC	771
OY	252	-----	252
Db	772	TGGGGCCCTAGACCCCTGGGGCTGAGACTGCCGGGGTGAGGCTGGGGATTCAAGGGGCG	831
OY	252	-----	252
Db	832	TACACTGCCGAGCGGAGAAAGAGCTGGGCTCCAGACAGCAGCCCTGGACTCTCTGTG	891
OY	253	-----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	270
Db	892	CAGTATCTCCACAGAAACTGAGAGTGAAGTGTTCCTCCAAAGCAAAACAGGACAGACTCTGGAA	951
OY	271	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValLys	290
Db	952	AACCTTGGGAGACGGCAGTCTCTCCAGTACTGAGAGGGCAAAAGCTGTGGCTGTCTGT	1011
OY	291	ValThrHisSerSerProProAlaArgLeuSerTTPThrGlnArgGlyGlnValLeuSer	310
Db	1012	GTACACACAGAGAGCCCCCAGCAGAGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC	1071
OY	311	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlnHisGlu	330
Db	1072	CCCTCCACACCCCTCAGACCCCGGGGCTCGGAGCTGCGTCGGGTTCAAGTGGAGCAGCA	1131
OY	331	GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	350
Db	1132	GGAAGATTCACTCCGACCGCTGGGACACCCACTGGGGCTCCAGACAGCTCTCTCAGCCTC	1191
OY	351	SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly	370
Db	1192	TTCGTGCACATTAAGAAAGGACTCATCTAACGGCATTTCTCCAAAGGAGCGTTTGGGA	1251

OY 371 IleglylethralaleuupheucysleuAlaleuilellewetysilleuPro 390
Db 1252 ATGGCATACAGGCTCTTCTTTCTCTCTGCGCCATATCATCTGAAGATTCTACCG 1311
OY 391 lysatgATgThglThrgluThrProarGProarGpseSerArgHisSerThrlleleu 410
Db 1312 AAGAGACGGACTCAGACAGAAACCCGAGCCAGGTTCTCCGGACAGCAGCATCTCG 1371
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Db 1612 AGACCAAGGCTCGAGGCGCGCATGCCCCAAGGCGACCCAGCGGATTCAGAGATCAAG 1671
OY 511 PheGln 512
Db 1672 TTCCAA 1677

RESULT 13
US-09-978-403A-258
Sequence 258, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250

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Best Local Similarity:	83.75%	Mismatches:	3
Query Match:	83.70%	Indels:	148
DB:	11	Gaps:	2

OY	1	MelleuLeuPProleuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaIleAspGlyArg	20
Db	46	ATGCTACTGCCACTGGCTGGCTTCGCGCGTGGGGGGGGTCCAGCGATGAGTGGAGA	105
OY	21	PhetrIleArgValGlnGlnSerValIleValProGlnGlyLeuCysIleSerValPro	40
Db	106	TTCTGGATACGAGATCGAGAGATCAGGATGGTCCGGAGGGCTGTGATCTCTGTGCC	165
OY	41	CysSerPheSerTyrProArgIleAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	60
Db	166	TGCTCTTTCTCCATACCCCGACAGACTGGACAGGGGTCTACCCCGATTAGCGCTACGG	225
OY	61	PheIlyAlaIleAlaThrGlnThrThrIlyrsGlyAlaProValAlaIleThrAsnHisGlnSerArg	80
Db	226	TTCAAGACACTGCTAGACAAACCAAGGGTGGTCTCTGTGGCCAAACCAACCAAGAGTCGA	285
OY	81	GluValGlnMetSerThrArgIlyArgPheGlnLeuThrGlyAspProAlaIlyGlyAsn	100
Db	286	GAGGTGAATATGACACCCGGGGCGGATTTCCAGTCACTGCGGGGATCCGCCAAGGGAGAC	345
OY	101	CysSerLeuValIleArgAspAlaGlnMetGlnAspGlnSerGlnTyrPhePheArgVal	120
Db	346	TGCTCTTGGTGATCGAGACCGCGCGAGATGACGAGTACAGTACTCTTTCCGGGTG	405
OY	121	GluArgGlySerTyrPalaArgTyrAsnPheMetAsnAspGlyPhePheLeuIlyValThr	140
Db	406	GAGAGAGGAAGCATATGTGACATPATAATTTCAAGAACAGATGGGTCTCTTTCAAAAGTAAACA	465
OY	141	AlaLeuThrGlnIlyProAspValTyrIleProGlnThrLeuGlnProGlyGlnProVal	160
Db	465	-----	465
OY	161	ThrValIleCysValPheAsnTrpAlaPheGlnGlnCysProProProSerPheSerTrp	180
Db	465	-----	465
OY	181	ThrGlyAlaAlaLeuSerSerGlnGlyThrIlyProThrIleSerHisPheSerValLeu	200
Db	466	-----GTCTTC	477
OY	201	SetPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	220
Db	472	AGCTTACGCCGACCCGACGACCAACACACACCGGACCTCAGCTGCATGTGAACTTCTCC	531
OY	221	ArgIlyGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp	240

Db 532 AGAAGGGTGTGAGCGCACAGAGACCGTCCGACTCCGTGTGGCCTATGCCCCAGAGAC 591
QY 241 LeuValIleSerIleSerArgPhePheProasp----- 252
Db 592 CTGTGTATCAGATTTCACGTGACACACAGCCCTGGAGCCCCAGCCCCAGGGAAT 651
QY 252 ----- 252
Db 652 GTCCCATACCTGGAGCCCAAGGCGCAGTTCCTGGGGCTCCTGTGTCTGTGACAGC 711
QY 252 ----- 252
Db 712 CAGCCCTGTGCACACTAGCTGGTCTCGACAAAGAGATCCTCTCTCTCCATCC 771
QY 252 ----- 252
Db 772 TGGGGCCTAGACCCCTGGGGCTGGAGCTGCCGGGGGTGAGGCTGGGGATTGAGGGCGC 831
QY 252 ----- 252
Db 832 TACACCTGCGAGCGGAGACAGGCTTGGCTCCAGACAGCGCCCTGGACCTCTGTG 891
QY 253 -----ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
Db 892 CAGTATCCTCCAGAGAACCTGAGAGTGTGTTTCCCAAGCAAGACAGGACAGTCTCGMA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuGlyValGly 290
Db 952 AACCTTGGGAAGCGACGCTCTCTCCAGTACTGGAGGGCAAGGCTGTGGCTGTCT 1011
QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyValGlnValLeuSer 310
Db 1012 GTCAACACACAGAGCGCCCGCCAGCGCTGAGCTGAGACCCAGAGGGGAGAGTTCTGAGC 1071
QY 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGlu 330
Db 1072 CCTCCAGACCCCTCAGACCCCGGGGCTCGAGAGTGTGCTCGGGTTCAAGTGAAGACGAA 1131
QY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
Db 1132 GGAGGTTCCACTGCGCAGCTGCGGACCCAGCTGGGCTCCACAGCGCTCTCTCGCC 1191
QY 351 SerValHisTrpLeuGlyGlyLeuLeuSerThrAlaPheSerAsnGlyValaPheLeuGly 370
Db 1192 TCCGCGCATATAAAGAGGACTCATCTCAAGGCAATCTCCAGCGAGCTTCTGGGA 1251
QY 371 IleGlyIleThrAlaLeuLeuPheLeuGlyLeuAlaLeuIleIleMetLysIleLeuPro 390
Db 1252 ATCCGATACAGGGCTCTTCTTCTCTGCTGGCCCTGATCATGAAATGTTCTACCG 1311
QY 391 LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu 410
Db 1312 AAGACAGGACTCAACAGAAACCCCGAGGGCCAGGTTCTCCGCGACAGCGATCTCCG 1371
QY 411 AspTrpIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430
Db 1372 GATTTCATCATGTGTGTCCCGAGCGCTGCGCCCTGGCTCAGAGCGGATAGAAAGCC 1431
QY 431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys 450
Db 1432 ACACCAAAACAGTCTCGAGCCCTCCACAGAGTGTGCTCCCGCAAAATCAACCAAGG 1491
QY 451 AsnGlnLysLysGlnTrpGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
Db 1492 AACCGAAAAACAGTATCATGTTGCCAGTTCCAGAAACCAAAATCAACCTCAAGCC 1551
QY 471 ProGluSerGlnIleSerGlnGluLeuLeuHisTrpAlaThrLeuAsnPheProGlyVal 490
Db 1552 CCAGAAATCCAGAGAGAGCCAGAGAGAGTCCATTATGCGACCGCTCACTCCAGAGCGTC 1611
QY 491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTrpAlaGluValLys 510
Db 1612 AGACCCAGGCGCTGAGGGCCGATGCCAAAGGCGACCCAGCGGATTTATGCAGAGTCAAG 1671

QY 511 PheGln 512
Db 1672 TTCCAA 1677
RESULT 14
US-09-978-564A-258
; Sequence 258, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroli, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavitt, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C25
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 9.93e-221 Length: 2764
Score: 2265.00 Matches: 450
Percent Similarity: 74.92% Conservative: 1
Best Local Similarity: 74.75% Mismatches: 3
Query Match: 83.70% Indels: 148
DB: 11 Gaps: 2

US-09-937-636-3 (1-512) x US-09-978-564A-258 (1-2764)

QY 1 MetLeuLeuProLeuLeuLeuSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20

DB 46 ATGCTACTGCCACTGCTGCTGCTGCTGCTGGGGGGTCCAGGCTATGATGGAGAGA 105
QY 21 PHEPTPIIEARyVALGIInLSerValMetValProGIUGLyLeucysIleSerValPro 40
DB 106 TTCTGGATACGAGTGCAGATGCATGATGCGCCGAGGGCTGTGCATCTCTGTGCCC 165
QY 41 CysSerPheSerTyProArgInAspTyrThrGlySerThrProAlaTyrGlyTyrTrp 60
DB 166 TCTCTCTTCTTCTTACCCCGACAGACTGGACGGGTCTTACCCCACTTATGGCTACTGG 225
QY 61 PheLysAlaValAlaThrGluThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80
DB 226 TTCAAAGCAGTGCATGACAGCAACCAAGGTGGTCCGTGGCCCAACCAACGAGATTCGA 285
QY 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
DB 286 GAGGTGGAAATAGCCACCGGGGGCGATTTCAGCTCAGTGGGATCCCGCAAGGGGAAC 345
QY 101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120
DB 346 TCTCTCTTGTGATTCAGACGCGGACGATGACAGATGAGTCAAGTACTTCTTGGGGTG 405
QY 121 GluArgGlySerTyValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
DB 406 GAGAGAGAAAGCTATGACATATATTTTCATGACAGCATGGGTCTTTTAAAGTAAACA 465
QY 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyLysProVal 160
DB 465 ----- 465
QY 161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180
DB 465 ----- 465
QY 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200
DB 466 -----GTGCTC 471
QY 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220
DB 472 ACCCTTCACGCCAGACCCCGAGACCCAGACCCGACCTCAGCTGCTGTGGCTCTCC 531
QY 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240
DB 532 AGAAAGGTGTGAGCCGACAGAGAGACCTCCGACTCTGTGCTTATGCCCCAGAGAC 591
QY 241 LeuValIleSerIleSerArgAspAsnThrProAsp----- 252
DB 592 CTGTGTATCAGCATTTTCAGTGACACAGCCAGCCCTGGAGCCCGCAGGGAAT 651
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DB 652 GTTCCATTACCTGGAAACCCAAAAGGCGAGTTCTGCGGCTCTGTGCTGTGACAGC 711
QY 252 ----- 252
DB 712 CAGCCCTGACCACTGAGTGGTCTGACAGAACAGATCTCTCTGTCCTCATTC 771
QY 252 ----- 252
DB 772 TGGGGCCCTAGACCCCTGGGCTGAGCTGCCGGGGGTGAAGGCTGGGATTCAGGGCGC 831
QY 252 ----- 252
DB 832 TACACCTGCCGAGCGGAGAAAGGCTTGGCTCCACAGCAGGAGCCCTGGACCTCTGTG 891
QY 253 -----ProGluLysAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270
DB 892 CAGTATCTCCAGAGAAACCTGAGAGTGAATGATGTTTCCCAAGCAACGACATGCTCGAA 951
QY 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyLysLeuValCys 290
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DB 952 AACCTTGGGAACGGCACGTCTCTCCAGTACTGAGAGGGCCAAAGCCTGTGCTGTCTGT 1011
QY 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyLysValLeuSer 310
DB 1012 GTTCACACAGAGAGCCCCCAGCAGGCTGAGCTGGACCCAAAGGGGAGGTCTGAGAC 1071
QY 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330
DB 1072 CCTCCACACCTCAGACACCCCGGGGTCTGAGACTCTCTCGGGTTCAATGGAGCAGCA 1131
QY 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350
DB 1132 GGAGATTCACCTGGCCACGCTGGGACCCACCTAGGGCTCCAGACAGTCTCTCAGCCTTC 1191
QY 351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370
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QY 391 LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu 410
DB 1312 AAGAGCGGACTCAGACAGAAACCCCGAGGCCAGGTCTCCCGGACAGCAGCATCTG 1371
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DB 1372 GATTACATCAATGTGTCTCCGACGGGTGCGCCCTGCTGCAGAAAGGGAATCAGAAAGCC 1431
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DB 1432 ACACCAAAAGTCTCGAGACCCCTCTCCACAGAGTGCTCCCTCCCAATCAAAAGAAAG 1491
QY 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470
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QY 471 ProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVal 490
DB 1552 CCAAGATCCAGAGAGGCCAAGAGAGCTTCATTATGCCAGCTCAACTCCAGGCGCTG 1611
QY 491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510
DB 1612 AGACCAAGGCTGAGAGGCCGAGATGCCCAAGGGCACCCAGCGGATTATGACAGATCAAG 1671
QY 511 PheGln 512
DB 1672 TTCCAA 1677
RESULT 15
US-09-999-833A-258
; Sequence 258, Application US/0999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999, 833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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